Figure 1
The Genetic Code

First Position (5' end)	Second position				Third position (3' end)
	U	C	A	G	
U	Phe	Ser	Tyr	Cys	U
	Phe	Ser	Tyr	Cys	C
	Leu	Ser	Stop	Stop	A
	Leu	Ser	Stop	Trp	G
C	Leu	Pro	His	Arg	U
	Leu	Pro	His	Arg	C
	Leu	Pro	Gln	Arg	A
	Leu	Pro	Gln	Arg	G
A	Ile	Thr	Asn	Ser	U
	Ile	Thr	Asn	Ser	C
	Ile	Thr	Lys	Arg	A
	Met	Thr	Lys	Arg	G
G	Val	Ala	Asp	Gly	U
	Val	Ala	Asp	Gly	C
	Val	Ala	Glu	Gly	A
	Val	Ala	Glu	Gly	G

Figure 2

```
GRVER51.SEQ  A T G A T G A A ● G C G A A A A G A A C G T G A T C ● C G G C C C A G A A C  40
GR6.SEQ      A T G A T G A A A C G C G A A A A G A A C G T G A T C T A C G G C C C A G A A C  40
GRVER5.SEQ   A T G A T G A A A C G C G A A A A G A A C G T G A T C T A C G G C C C A G A A C  40
GRVER4.SEQ   A T G A T G A A A C G C G A A A A G A A C G T G A T C T A C G G C C C A G A A C  40
GRVER3.SEQ   A T G A T G A A A C G C G A A A A G A A C G T G A T C T A C G G C C C A G A A C  40
GRVER2.SEQ   A T G A T G A A A C G C G A A A A G A A C G T C A T C T A C G G C C C A G A G C  40
GRVER1.SEQ   A T G A T G A A A C G C G A A A A G A A C G T C A T C T A C G G C C C A G A G C  40
YG81-6G1.SEQ A T G A T G A A G C G A G A G A A A A A T G T T A T A T A T G G A C C C G A A C  40
RDVER1.SEQ   A T G A T G A A G C G T G A G A A A A A T G T G A T T T A T G G T C C T G A A C  40
RDVER2.SEQ   A T G A T G A A G C G T G A G A A A A A T G T G A T T T A T G G T C C T G A A C  40
RDVER3.SEQ   A T G A T G A A G C G T G A G A A A A A T G T C A T C T A T G G C C C T G A G C  40
RDVER4.SEQ   A T G A T G A A G C G T G A G A A A A A T G T C A T C T A T G G C C C T G A G C  40
RDVER5.SEQ   A T G A T G A A G C G T G A G A A A A A T G T C A T C T A T G G C C C T G A G C  40
RD7.SEQ      A T G A T G A A G C G T G A G A A A A A T G T C A T C T A T G G C C C T G A G C  40
RDVER51.SEQ  A T G A T G A A G C G T G A G A A A A A T G T C A T C T A T G G C C C T G A G C  40
RDVER52.SEQ  A T G A T G A A G C G T G A G A A A A A T G T C A T C T A T G G C C C T G A G C  40
RD1561H9.SEQ A T G A T A A A G C G T G A G A A A A A T G T C A T C T A T G G C C C T G A G C  40

GRVER51.SEQ  C A C T G C A T C C A C T G G A A G A C C T C A C C G C T G G T G A G A T G C T  80
GR6.SEQ      C A C T G C A T C C A C T G G A A G A C C T C A C C G C T G G T G A G A T G C T  80
GRVER5.SEQ   C A C T G C A T C C A C T G G A A G A C C T C A C C G C T G G T G A G A T G C T  80
GRVER4.SEQ   C A C T G C A T C C A C T G G A A G A C C T C A C C G C T G G T G A G A T G C T  80
GRVER3.SEQ   C A C T G C A T C C A C T G G A A G A C C T C A C C G C T G G T G A G A T G C T  80
GRVER2.SEQ   C T C T G C A C C C A T T G G A A G A C C T G A C C G C T G G T G A G A T G T T  80
GRVER1.SEQ   C T C T G C A C C C A T T G G A A G A C C T G A C C G C C G G T G A G A T G T T  80
YG81-6G1.SEQ C C C T A C A C C C C T T G G A A G A C T T A A C A G C T G G A G A A A T G C T  80
RDVER1.SEQ   C A T T G C A T C C T C T G G A G G A T T T G A C T G C T G G C G A A A T G C T  80
RDVER2.SEQ   C A T T G C A T C C T C T G G A G G A T T T G A C T G C C G G C G A A A T G C T  80
RDVER3.SEQ   C T T T G C A C C C T T T G G A G G A T T T G A C T G C C G G C G A A A T G C T  80
RDVER4.SEQ   C T T T G C A T C C T T T G G A G G A T T T G A C T G C C G G C G A A A T G C T  80
RDVER5.SEQ   C T C T C C A T C C T T T G G A G G A T T T G A C T G C C G G C G A A A T G C T  80
RD7.SEQ      C T C T C C A T C C T T T G G A G G A T T T G A C T G C C G G C G A A A T G C T  80
RDVER51.SEQ  C T C T C C A T C C T T T G G A G G A T T T G A C T G C C G G C G A A A T G C T  80
RDVER52.SEQ  C T C T C C A T C C T T T G G A G G A T T T G A C T G C C G G C G A A A T G C T  80
RD1561H9.SEQ C T C T C C A T C C T T T G G A G G A T T T G A C T G C C G G C G A A A T G C T  80

GRVER51.SEQ  C T T C C G A G C A C T G C G T A A A C A T A G T C A C C T C C C T C A A G C A  120
GR6.SEQ      C T T C C G A G C A C T G C G T A A A C A T A G T C A C C T C C C T C A A G C A  120
GRVER5.SEQ   C T T C C G A G C A C T G C G T A A A C A T A G T C A C C T C C C T C A A G C A  120
GRVER4.SEQ   C T T C C G T G C A C T G C G T A A A C A T A G T C A C C T C C C T C A A G C T  120
GRVER3.SEQ   G T T C C G T G C C C T G C G T A A A C A T A G C C A C C T G C C T C A A G C T  120
GRVER2.SEQ   G T T C C G T G C T C T G C G T A A A C A T T C T C A C T T G C C T C A A G C C  120
GRVER1.SEQ   G T T C C G T G C T C T G C G T A A A C A T T C T C A C T T G C C T C A A G C C  120
YG81-6G1.SEQ C T T C C G T G C C C T T C G A A A A C A T T C T C A T T T A C C G C A G G C T  120
RDVER1.SEQ   G T T T C G C G C C T T G C G C A A G C A C A G C C A T C T G C C A C A G G C T  120
RDVER2.SEQ   G T T T C G C G C C T T G C G C A A G C A C A G C C A T C T G C C A C A A G C T  120
RDVER3.SEQ   G T T T C G C G C T T T G C G T A A G C A C T C T C A T T T G C C T C A A G C C  120
RDVER4.SEQ   G T T T C G T G C T T T G C G T A A A C A C T C T C A T T T G C C T C A A G C C  120
RDVER5.SEQ   G T T T C G T G C T C T C C G C A A G C A C T C T C A T T T G C C T C A A G C C  120
RD7.SEQ      G T T T C G T G C T C T C C G C A A G C A C T C T T A T T T G C C T C A A G C C  120
RDVER51.SEQ  G T T T C G T G C T C T C C G C A A G C A C T C T C A T T T G C C T C A A G C C  120
RDVER52.SEQ  G T T T C G T G C T C T C C G C A A G C A C T C T C A T T T G C C T C A A G C C  120
RD1561H9.SEQ G T T T C G T G C T C T C C G C A A G C A C T C T C A T T T G C C T C A A G C C  120
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Figure 2 (cont.)

```
GRVER51.SEQ  C T C G T G G A   T C G T G G G A G A C G A G A G C   C T C C T A C A A A G  160
GR6.SEQ      C T C G T G G A C G T C G T G G G A G A C G A G A A C C T C T C C T A C A A A G  160
GRVER5.SEQ   C T C G T G G A C G T C G T G G G A G A C G A G A G C C T C T C C T A C A A A G  160
GRVER4.SEQ   C T C G T G G A C G T C G T G G G A G A C G A G A G C C T C T C T T A C A A A G  160
GRVER3.SEQ   C T C G T G G A C G T C G T G G G T G A C G A G A G C C T G T C T T A C A A A G  160
GRVER2.SEQ   C T G G T C G A T G T C G T G G G C G A C G A G A G C T T G T C T T A T A A G G  160
GRVER1.SEQ   C T G G T G G A T G T C G T G G G C G A C G A A A G C T T G T C T T A T A A G G  160
YG81-6G1.SEQ T T A G T A G A T G T G G T T G G C G A C G A A T C G C T T T C C T A T A A A G  160
RDVER1.SEQ   T T G G T C G A C G T G G T C G G T G A T G A G T C T C T G A G C T A C A A A G  160
RDVER2.SEQ   T T G G T C G G A C G T G G T C G G T G A T G A A T C T C T G A G C T A C A A A G  160
RDVER3.SEQ   T T G G T C G A T G T G G T C G G C G A T G A A T C T T T G A G C T A T A A G G  160
RDVER4.SEQ   T T G G T C G A T G T G G T C G G C G A T G A A T C T T T G A G C T A C A A G G  160
RDVER5.SEQ   T T G G T C G A T G T G G T C G G C G A T G A A T C T T T G A G C T A C A A G G  160
RD7.SEQ      T T G G T C G A T G T G G T C G G C G A T G A A T C T T T G A G C T A C A A G G  160
RDVER51.SEQ  T T G G T C G A T G T G G T C G G C G A T G A A T C T T T G A G C T A C A A G G  160
RDVER52.SEQ  T T G G T C G A T G T G G T C G G C G A T G A A T C T T T G A G C T A C A A G G  160
RD1561H9.SEQ T T G G T C G A T G T G G T C G G C G A T G A A T C T T T G A G C T A C A A G G  160


GRVER51.SEQ  A A T T T T T C G A A G C T A C T G T G C T G T T G G C C C A A A G C C T C C A  200
GR6.SEQ      A A T T T T T C G A A G C T A C T G T G C T G T T G G C C C A A A G C C T C C A  200
GRVER5.SEQ   A A T T T T T C G A A G C T A C T G T G C T G T T G G C C C A A A G C C T C C A  200
GRVER4.SEQ   A A T T T T T C G A A G C T A C T G T G C T G T T G G C C C A A A G C C T C C A  200
GRVER3.SEQ   A A T T T T T C G A A G C T A C T G T G C T G T T G G C C C A A A G C C T G C A  200
GRVER2.SEQ   A A T T T T T C G A A G C T A C T G T C C T G T T G G C C C A A T C T C T G C A  200
GRVER1.SEQ   A G T T T T T C G A A G C T A C T G T C C T G T T G G C C C A G T C T C T G C A  200
YG81-6G1.SEQ A G T T T T T T G A A G C G A C A G T C C T C C T A G C G C A A A G T C T C C A  200
RDVER1.SEQ   A A T T C T T T G A G G C C A C C G T G T T G C T G G C T C A A A G C T T G C A  200
RDVER2.SEQ   A G T T C T T T G A G G C A A C C G T G T T G C T G G C T C A G A G C T T G C A  200
RDVER3.SEQ   A G T T T T T T G A G G C A A C C G T C T T G C T G G C T C A G T C T T T G C A  200
RDVER4.SEQ   A G T T T T T T G A G G C A A C C G T C T T G C T G G C T C A G T C C T T G C A  200
RDVER5.SEQ   A G T T T T T T G A G G C A A C C G T C T T G C T G G C T C A G T C C C T C C A  200
RD7.SEQ      A G T T T T T T G A G G C A A C C G T C T T G C T G G C T C A G T C C C T C C A  200
RDVER51.SEQ  A G T T T T T T G A G G C A A C C G T C T T G C T G G C T C A G T C C C T C C A  200
RDVER52.SEQ  A G T T T T T T G A G G C A A C C G T C T T G C T G G C T C A G T C C C T C C A  200
RD1561H9.SEQ A G T T T T T T G A G G C A A C C G T C T T G C T G G C T C A G T C C C T C C A  200


GRVER51.SEQ  T A A T T G T G G G T A C A A A A T G A A C G A T G T G G T G A G C A T T T G T  240
GR6.SEQ      T A A T T G T G G G T A C A A A A T G A A C G A T G T G G T G A G C A T T T G T  240
GRVER5.SEQ   T A A T T G T G G G T A C A A A A T G A A C G A T G T G G T G A G C A T T T G T  240
GRVER4.SEQ   T A A T T G T G G A T A C A A A A T G A A C G A T G T G G T G A G C A T T T G T  240
GRVER3.SEQ   T A A T T G T G G T T A C A A A A T G A A C G A T G T G G T G A G C A T C T G T  240
GRVER2.SEQ   T A A T T G C G G T T A C A A A A T G A A C G A T G T G G T C A G C A T T T G T  240
GRVER1.SEQ   T A A T T G C G G T T A C A A A A T G A A C G A T G T G G T C A G C A T T T G T  240
YG81-6G1.SEQ C A A T T G T G G A T A C A A G A T G A A T G A T G T A G T G T C G A T C T G C  240
RDVER1.SEQ   C A A C T G T G G C T A T A A G A T G A A T G A C G T C G T G T C T A T C T G C  240
RDVER2.SEQ   C A A C T G T G G C T A T A A G A T G A A T G A C G T C G T G T C T A T C T G C  240
RDVER3.SEQ   T A A T T G C G G C T A C A A G A T G A A C G A C G T C G T C T C T A T T T G T  240
RDVER4.SEQ   T A A T T G T G G C T A C A A G A T G A A C G A C G T C G T C T C C A T T T G T  240
RDVER5.SEQ   C A A T T G T G G C T A C A A G A T G A A C G A C G T C G T T A G T A T C T G T  240
RD7.SEQ      C A A T T G T G G C T A C A A G A T G A A C G A C G T C G T T A G T A T C T G T  240
RDVER51.SEQ  C A A T T G T G G C T A C A A G A T G A A C G A C G T C G T T A G T A T C T G T  240
RDVER52.SEQ  C A A T T G T G G C T A C A A G A T G A A C G A C G T C G T T A G T A T C T G T  240
RD1561H9.SEQ C A A T T G T G G C T A C A A G A T G A A C G A C G T C G T T A G T A T C T G T  240
```

Figure 2 (cont.)

```
GRVER51.SEQ   G C T G A G A A    A C A C T C G C T T C T T T A T T C    G T A A T C G C T G 280
GR6.SEQ       G C T G A G A A T A A C A C T C G C T T C T T T A T T C C T G T A A T C G C T G 280
GRVER5.SEQ    G C T G A G A A T A A C A C T C G C T T C T T T A T T C C T G T A A T C G C T G 280
GRVER4.SEQ    G C T G A G A A T A A C A C T C G C T T C T T T A T C C C T G T T A T C G C T G 280
GRVER3.SEQ    G C T G A G A A T A A C A C T C G C T T T T T T A T C C C T G T G A T C G C T G 280
GRVER2.SEQ    G C T G A G A A T A A C A C C C G C T T T T T C A T C C C A G T G A T T G C C G 280
GRVER1.SEQ    G C T G A G A A T A A C A C C C G C T T T T T C A T C C C A G T G A T T G C C G 280
YG81-6G1.SEQ  G C C G A G A A T A A T A C A A G A T T T T T T A T T C C C G T T A T T G C A G 280
RDVER1.SEQ    G C C G A A A C A A T A C T C G T T T C T T T A T T C C T G T C A T C G C T G 280
RDVER2.SEQ    G C C G A A A C A A T A C T C G T T T C T T T A T T C C T G T C A T C G C T G 280
RDVER3.SEQ    G C C G A A A C A A T A C C C G T T T C T T C A T T C C A G T C A T C G C C G 280
RDVER4.SEQ    G C A G A A A C A A T A C C C G T T T C T T C A T T C C A G T C A T C G C C G 280
RDVER5.SEQ    G C T G A A A C A A T A C C C G T T T C T T C A T T C C A G T C A T C G C C G 280
RD7.SEQ       G C T G A A A C A A T A C C C G T T T C T T C A T T C C A G T C A T C G C C G 280
RDVER51.SEQ   G C T G A A A C A A T A C C C G T T T C T T C A T T C C A G T C A T C G C C G 280
RDVER52.SEQ   G C T G A A A C A A T A C C C G T T T C T T C A T T C C A G T C A T C G C C G 280
RD1561H9.SEQ  G C T G A A A C A A T A C C C G T T T C T T C A T T C C A G T C A T C G C C G 280

GRVER51.SEQ   C T T G G T A C A T C G G C A T G A T T G T C G C C C C T G T G A A T G A A T C 320
GR6.SEQ       C T T G G T A C A T C G G C A T G A T T G T C G C C C C T G T G A A T G A A T C 320
GRVER5.SEQ    C T T G G T A C A T C G G C A T G A T T G T C G C C C C T G T G A A T G A A T C 320
GRVER4.SEQ    C T T G G T A C A T C G G C A T G A T T G T C G C C C C T G T G A A T G A A T C 320
GRVER3.SEQ    C T T G G T A C A T C G G C A T G A T T G T C G C C C C T G T G A A T G A A T C 320
GRVER2.SEQ    C T T G G T A C A T C G G C A T G A T T G T C G C C C C T G T G A A T G A A T C 320
GRVER1.SEQ    C T T G G T A C A T C G G C A T G A T T G T C G C C C C T G T G A A T G A A T C 320
YG81-6G1.SEQ  C T T G G T A T A T T G G T A T G A T T G T A G C A C C T G T T A A T G A A A G 320
RDVER1.SEQ    C C T G G T A T A T T G G T A T G A T C G T G G C T C C A G T C A A C G A G A G 320
RDVER2.SEQ    C C T G G T A T A T T G G T A T G A T C G T G G C T C C A G T C A A C G A G A G 320
RDVER3.SEQ    C C T G G T A T A T C G G T A T G A T C G T G G C T C C A G T C A A C G A G A G 320
RDVER4.SEQ    C A T G G T A T A T C G G T A T G A T C G T G G C T C C A G T C A A C G A G A G 320
RDVER5.SEQ    C A T G G T A T A T C G G T A T G A T C G T G G C T C C A G T C A A C G A G A G 320
RD7.SEQ       C A T G G T A T A T C G G T A T G A T C G T G G C T C C A G T C A A C G A G A G 320
RDVER51.SEQ   C A T G G T A T A T C G G T A T G A T C G T G G C T C C A G T C A A C G A G A G 320
RDVER52.SEQ   C A T G G T A T A T C G G T A T G A T C G T G G C T C C A G T C A A C G A G A G 320
RD1561H9.SEQ  C A T G G T A T A T C G G T A T G A T C G T G G C T C C A G T C A A C G A G A G 320

GRVER51.SEQ   T T A C A T C C C A G A T G A G C T G T G T A A G G T T A T G G G T A T T A G C 360
GR6.SEQ       T T A C A T C C C A G A T G A G C T G T G T A A G G T T A T G G G T A T T A G C 360
GRVER5.SEQ    T T A C A T C C C A G A T G A G C T G T G T A A G G T T A T G G G T A T T A G C 360
GRVER4.SEQ    T T A C A T C C C A G A T G A G C T G T G T A A G G T T A T G G G T A T T A G C 360
GRVER3.SEQ    T T A C A T C C C A G A T G A G T T G T G T A A G G T G A T G G G T A T T A G C 360
GRVER2.SEQ    T T A T A T C C C A G A C G A G T T G T G C A A G G T C A T G G G T A T T A G C 360
GRVER1.SEQ    T T A T A T C C C A G A C G A G T T G T G C A A G G T C A T G G G T A T T A G C 360
YG81-6G1.SEQ  T T A C A T C C C A G A T G A A C T C T G T A A G G T G A T G G G T A T A T C G 360
RDVER1.SEQ    C T A C A T T C C T G A T G A A C T G T G T A A A G T G A T G G G C A T C T C T 360
RDVER2.SEQ    C T A C A T T C C T G A T G A A C T G T G T A A A G T G A T G G G C A T C T C T 360
RDVER3.SEQ    C T A C A T T C C T G A C G A A C T G T G T A A A G T C A T G G G T A T C T C T 360
RDVER4.SEQ    C T A C A T T C C C G A C G A A C T G T G T A A A G T C A T G G G T A T C T C T 360
RDVER5.SEQ    C T A C A T T C C C G A C G A A C T G T G T A A A G T C A T G G G T A T C T C T 360
RD7.SEQ       C T A C A T T C C C G A C G A A C T G T G T A A A G T C A T G G G T A T C T C T 360
RDVER51.SEQ   C T A C A T T C C C G A C G A A C T G T G T A A A G T C A T G G G T A T C T C T 360
RDVER52.SEQ   C T A C A T T C C C G A C G A A C T G T G T A A A G T C A T G G G T A T C T C T 360
RD1561H9.SEQ  C T A C A T T C C C G A C G A A C T G T G T A A A G T C A T G G G T A T C T C T 360
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Figure 2 (cont.)

```
GRVER51.SEQ   A A A C C T C A ● A T C G T C T T T A C T A C C A A A ● C A T C T T G A A T A   400
GR6.SEQ       A A A C C T C A A A T C G T C T T T A C T A C C A A A A A C A T C T T G A A T A   400
GRVER5.SEQ    A A A C C T C A A A T C G T C T T T A C T A C C A A A A A C A T C T T G A A T A   400
GRVER4.SEQ    A A A C C T C A A A T C G T C T T T A C T A C C A A A A A T A T C C T G A A T A   400
GRVER3.SEQ    A A A C C T C A A A T C G T C T T T A C T A C C A A A A A C A T C C T G A A T A   400
GRVER2.SEQ    A A A C C T C A A A T C G T G T T T A C T A C C A A G A A C A T T C T G A A T A   400
GRVER1.SEQ    A A A C C T C A A A T C G T G T T T A C T A C C A A G A A C A T T C T G A A T A   400
YG81-6G1.SEQ  A A A C C A C A A A T A G T T T T T A C G A C A A A G A A C A T T T T A A A T A   400
RDVER1.SEQ    A A G C C A C A G A T T G T C T T C A C C A C T A A A A A T A T C T T G A A C A   400
RDVER2.SEQ    A A G C C A C A G A T T G T C T T C A C C A C T A A A A A T A T C T T G A A C A   400
RDVER3.SEQ    A A G C C A C A G A T T G T G T T C A C C A C T A A G A A T A T T T T G A A C A   400
RDVER4.SEQ    A A G C C A C A G A T T G T C T T C A C C A C T A A G A A T A T T C T G A A C A   400
RDVER5.SEQ    A A G C C A C A G A T T G T C T T C A C C A C T A A G A A T A T T C T G A A C A   400
RD7.SEQ       A A G C C A C A G A T T G T C T T C A C C A C T A A G A A T A T T C T G A A C A   400
RDVER51.SEQ   A A G C C A C A G A T T G T C T T C A C C A C T A A G A A T A T T C T G A A C A   400
RDVER52.SEQ   A A G C C A C A G A T T G T C T T C A C C A C T A A G A A T A T T C T G A A C A   400
RD1561H9.SEQ  A A G C C A C A G A T T G T C T T C A C C A C T A A G A A T A T T C T G A A C A   400


GRVER51.SEQ   A G G T C T T G G A A G T C C A G T C T C G T A C T A A C T T C A T C A A A C G   440
GR6.SEQ       A G G T C T T G G A A G T C C A G T C T C G T A C T A A C T T C A T C A A A C G   440
GRVER5.SEQ    A G G T C T T G G A A G T C C A G T C T C G T A C T A A C T T C A T C A A A C G   440
GRVER4.SEQ    A G G T C T T G G A A G T C C A G T C T C G T A C T A A C T T C A T C A A A C G   440
GRVER3.SEQ    A G G T C T T G G A A G T C C A G T C T C G T A C T A A T T T C A T C A A A C G   440
GRVER2.SEQ    A G G T C T T G G A A G T G C A G T C T C G T A C T A A C T T C A T C A A G C G   440
GRVER1.SEQ    A A G T C T T G G A A G T G C A G T C T C G T A C T A A C T T C A T C A A G C G   440
YG81-6G1.SEQ  A G G T A T T G G A G G T A C A G A G C A G A A C T A A T T T C A T A A A A A G   440
RDVER1.SEQ    A G G T G C T G G A G G T C C A A A G C C G C A C C A A T T T T A T T A A A C G   440
RDVER2.SEQ    A A G T G C T G G A G G T C C A A A G C C G C A C C A A C T T T A T T A A G C G   440
RDVER3.SEQ    A A G T G C T G G A A G T C C A A A G C C G C A C C A A C T T T A T T A A G C G   440
RDVER4.SEQ    A A G T C C T G G A A G T C C A A A G C C G C A C C A A C T T T A T T A A G C G   440
RDVER5.SEQ    A A G T C C T G G A A G T C C A A A G C C G C A C C A A C T T T A T T A A G C G   440
RD7.SEQ       A A G T C C T G G A A G T C C A A A G C C G C A C C A A C T T T A T T A A G C G   440
RDVER51.SEQ   A A G T C C T G G A A G T C C A A A G C C G C A C C A A C T T T A T T A A G C G   440
RDVER52.SEQ   A A G T C C T G G A A G T C C A A A G C C G C A C C A A C T T T A T T A A G C G   440
RD1561H9.SEQ  A A G T C C T G G A A G T C C A A A G C C G C A C C A A C T T T A T T A A G C G   440


GRVER51.SEQ   C A T C A T T A T T C T G G A T A C C G T C G A A A A C A T C C A C G G C T G T   480
GR6.SEQ       C A T C A T T A T T C T G G A T A C C G T C G A A A A C A T C C A C G G C T G T   480
GRVER5.SEQ    C A T C A T T A T T C T G G A T A C C G T C G A A A A C A T C C A C G G C T G T   480
GRVER4.SEQ    C A T C A T T A T T C T G G A T A C C G T C G A A A A C A T C C A T G G C T G T   480
GRVER3.SEQ    C A T T A T T A T T C T G G A T A C C G T C G A A A A C A T C C A C G G C T G T   480
GRVER2.SEQ    C A T T A T C A T T C T G G A T A C C G T C G A G A A T A T C C A C G G C T G T   480
GRVER1.SEQ    C A T T A T C A T T C T G G A T A C C G T C G A G A A T A T C C A C G G C T G T   480
YG81-6G1.SEQ  G A T C A T C A T A C T T G A T A C T G T A G A A A A C A T A C A C G G T T G T   480
RDVER1.SEQ    T A T C A T T A T C T T G G A C A C T G T G G A A A A C A T T C A T G G T T G C   480
RDVER2.SEQ    T A T C A T T A T C T T G G A C A C T G T G G A A A A C A T T C A T G G T T G C   480
RDVER3.SEQ    T A T C A T C A T C T T G G A C A C T G T G G A G A A T A T T C A C G G T T G C   480
RDVER4.SEQ    T A T C A T C A T C T T G G A C A C T G T G G A G A A T A T T C A C G G T T G C   480
RDVER5.SEQ    T A T C A T C A T C T T G G A C A C T G T G G A G A A T A T T C A C G G T T G C   480
RD7.SEQ       T A T C A T C A T C T T G G A C A C T G T G G A G A A T A T T C A C G G T T G C   480
RDVER51.SEQ   T A T C A T C A T C T T G G A C A C T G T G G A G A A T A T T C A C G G T T G C   480
RDVER52.SEQ   T A T C A T C A T C T T G G A C A C T G T G G A G A A T A T T C A C G G T T G C   480
RD1561H9.SEQ  T A T C A T C A T C T T G G A C A C T G T G G A G A A T A T T C A C G G T T G C   480
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Figure 2 (cont.)

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GRVER51.SEQ   G A G A G C C T ● C T A A C T T C A T C T C T C G T T ● A G C G A T G G T A 520
GR6.SEQ       G A G A G C C T C C C T A A C T T C A T C T C T C G T T A C A G C G A T G G T A 520
GRVER5.SEQ    G A G A G C C T C C C T A A C T T C A T C T C T C G T T A C A G C G A T G G T A 520
GRVER4.SEQ    G A G A G C C T G C C T A A C T T C A T C T C T C G T T A C A G C G A T G G T A 520
GRVER3.SEQ    G A G A G C T T G C C T A A C T T T A T C T C T C G T T A C A G C G A T G G T A 520
GRVER2.SEQ    G A G A G C T T G C C A A A C T T T A T T T C T C G T T A T A G C G A C G G T A 520
GRVER1.SEQ    G A A A G C T T G C C A A A C T T T A T T T C T C G T T A T A G C G A C G G T A 520
YG81-6G1.SEQ  G A A A G T C T T C C C A A T T T T A T T T C T C G T T A T T C G G A T G G A A 520
RDVER1.SEQ    G A G T C T C T G C C T A A T T T C A T C A G C C G C T A C T C T G A T G G C A 520
RDVER2.SEQ    G A A T C T C T G C C T A A T T T C A T C A G C C G C T A C T C T G A T G G C A 520
RDVER3.SEQ    G A A T C T C T G C C T A A T T T C A T T A G C C G C T A T T C T G A C G G C A 520
RDVER4.SEQ    G A A T C T T T G C C T A A T T T T A T T A G C C G C T A T T C A G A C G G A A 520
RDVER5.SEQ    G A A T C T T T G C C T A A T T T C A T C T C T C G C T A T T C A G A C G G C A 520
RD7.SEQ       G A A T C T T T G C C T A A T T T C A T C T C T C G C T A T T C A G A C G G C A 520
RDVER51.SEQ   G A A T C T T T G C C T A A T T T C A T C T C T C G C T A T T C A G A C G G C A 520
RDVER52.SEQ   G A A T C T T T G C C T A A T T T C A T C T C T C G C T A T T C A G A C G G C A 520
RD1561H9.SEQ  G A A T C T T T G C C T A A T T T C A T C T C T C G C T A T T C A G A C G G C A 520


GRVER51.SEQ   A T A T C G C T A A T T T C A A G C C C T T G C A T T T T G A T C C A G T C G A 560
GR6.SEQ       A T A T C G C T A A T T T C A A G C C C T T G C A T T T T G A T C C A G T C G A 560
GRVER5.SEQ    A T A T C G C T A A T T T C A A G C C C T T G C A T T T T G A T C C A G T C G A 560
GRVER4.SEQ    A T A T C G C T A A T T T C A A A C C A C T G C A T T T T G A T C C A G T C G A 560
GRVER3.SEQ    A T A T C G C T A A T T T C A A G C C A C T G C A T T T T G A T C C A G T C G A 560
GRVER2.SEQ    A T A T C G C T A A C T T C A A G C C T C T G C A T T T T G A T C C A G T G G A 560
GRVER1.SEQ    A T A T C G C T A A C T T C A A G C C T C T G C A T T T T G A T C C A G T G G A 560
YG81-6G1.SEQ  A T A T T G C C A A C T T C A A A C C T T T A C A T T T C G A T C C T G T T G A 560
RDVER1.SEQ    A C A T T G C C A A T T T T A A A C C A T T G C A C T T C G A C C C T G T C G A 560
RDVER2.SEQ    A C A T T G C C A A T T T T A A A C C A T T G C A C T T C G A C C C T G T C G A 560
RDVER3.SEQ    A C A T C G C C A A C T T T A A A C C T T T G C A T T T C G A C C C T G T G G A 560
RDVER4.SEQ    A C A T C G C C A A C T T T A A G C C T C T C C A T T T C G A C C C T G T G G A 560
RDVER5.SEQ    A C A T C G C A A A C T T T A A A C C A C T C C A C T T C G A C C C T G T G G A 560
RD7.SEQ       A C A T C G C A A A C T T T A A A C C A C T C C A C T T C G A C C C T G T G G A 560
RDVER51.SEQ   A C A T C G C A A A C T T T A A A C C A C T C C A C T T C G A C C C T G T G G A 560
RDVER52.SEQ   A C A T C G C A A A C T T T A A A C C A C T C C A C T T C G A C C C T G T G G A 560
RD1561H9.SEQ  A C A T C G C A A A C T T T A A A C C A C T C C A C T T C G A C C C T G T G G A 560


GRVER51.SEQ   G C A A G T G G C C G C T A T T T T G T G C T C C T C C G G C A C C A C T G G T 600
GR6.SEQ       G C A A G T G G C C G C T A T T T T G T G C T C C T C C G G C A C C A C T G G T 600
GRVER5.SEQ    G C A A G T G G C C G C T A T T T T G T G C T C C T C C G G C A C C A C T G G T 600
GRVER4.SEQ    G C A A G T G G C C G C T A T T T T G T G C T C T T C C G G C A C C A C T G G T 600
GRVER3.SEQ    G C A G G T C G C C G C C A T T T T G T G C T C T T C T G G C A C C A C T G G T 600
GRVER2.SEQ    G C A A G T C G C C G C T A T T T T G T G C T C T A G C G G C A C C A C C G G T 600
GRVER1.SEQ    G C A A G T C G C C G C T A T T T T G T G C T C T A G C G G C A C T A C C G G T 600
YG81-6G1.SEQ  G C A A G T G G C A G C T A T C T T A T G T T C G T C A G G C A C T A C T G G A 600
RDVER1.SEQ    A C A G G T G G C T G C C A T C C T G T G T A G C T C T G G T A C C A C T G G C 600
RDVER2.SEQ    A C A G G T G G C T G C C A T C C T G T G T A G C T C T G G T A C T A C T G G C 600
RDVER3.SEQ    A C A A G T G G C T G C T A T C C T G T G T A G C A G C G G T A C T A C T G G C 600
RDVER4.SEQ    A C A A G T T G C T G C A A T C C T G T G T A G C A G C G G T A C T A C T G G A 600
RDVER5.SEQ    A C A A G T T G C A G C C A T T C T G T G T A G C A G C G G T A C T A C T G G A 600
RD7.SEQ       A C A A G T T G C A G C C A T T C T G T G T A G C A G C G G T A C T A C T G G A 600
RDVER51.SEQ   A C A A G T T G C A G C C A T T C T G T G T A G C A G C G G T A C T A C T G G A 600
RDVER52.SEQ   A C A A G T T G C A G C C A T T C T G T G T A G C A G C G G T A C T A C T G G A 600
RD1561H9.SEQ  A C A A G T T G C A G C C A T T C T G T G T A G C A G C G G T A C T A C T G G A 600
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Figure 2 (cont.)

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GRVER51.SEQ  T T G C C T A A ● G T G T C A T G C A G A C T C A C C ● A A T A T C T G T G  640
GR6.SEQ      T T G C C T A A A G G T G T C A T G C A G A C T C A C C A G A A T A T C T G T G  640
GRVER5.SEQ   T T G C C T A A A G G T G T C A T G C A G A C T C A C C A G A A T A T C T G T G  640
GRVER4.SEQ   T T G C C T A A A G G T G T C A T G C A G A C T C A C C A G A A T A T C T G T G  640
GRVER3.SEQ   T T G C C T A A A G G T G T C A T G C A G A C T C A C C A G A A T A T C T G T G  640
GRVER2.SEQ   C T G C C T A A A G G C G T G A T G C A G A C T C A C C A A A A T A T C T G T G  640
GRVER1.SEQ   C T G C C T A A A G G C G T G A T G C A G A C T C A C C A A A A T A T C T G T G  640
YG81-6G1.SEQ T T A C C G A A A G G T G T A A T G C A A A C T C A C C A A A A T A T T T G T G  640
RDVER1.SEQ   T T G C C A A A G G G T G T C A T G C A A A C C C A T C A G A A C A T T T G C G  640
RDVER2.SEQ   T T G C C A A A G G G T G T C A T G C A A A C C C A T C A G A A C A T T T G C G  640
RDVER3.SEQ   C T C C C A A A G G G C G T C A T G C A G A C C C A T C A A A A C A T T T G C G  640
RDVER4.SEQ   C T C C C A A A G G G A G T C A T G C A G A C C C A T C A A A A C A T T T G C G  640
RDVER5.SEQ   C T C C C A A A G G G A G T C A T G C A G A C C C A T C A A A A C A T T T G C G  640
RD7.SEQ      C T C C C A A A G G G A G T C A T G C A G A C C C A T C A A A A C A T T T G C G  640
RDVER51.SEQ  C T C C C A A A G G G A G T C A T G C A G A C C C A T C A A A A C A T T T G C G  640
RDVER52.SEQ  C T C C C A A A G G G A G T C A T G C A G A C C C A T C A A A A C A T T T G C G  640
RD1561H9.SEQ C T C C C A A A G G G A G T C A T G C A G A C C C A T C A A A A C A T T T G C G  640

GRVER51.SEQ  T G C G T T T G A T C C A C G C T C T C G A C C C T C G T G T G G G T A C T C A  680
GR6.SEQ      T G C G T T T G A T C C A C G C T C T C G A C C C T C G T G T G G G T A C T C A  680
GRVER5.SEQ   T G C G T T T G A T C C A C G C T C T C G A C C C T C G T G T G G G T A C T C A  680
GRVER4.SEQ   T G C G T T T G A T C C A C G C T C T C G A C C C T C G T G T G G G T A C T C A  680
GRVER3.SEQ   T G C G C T T G A T C C A C G C C C T C G A C C C T C G T G T G G G T A C T C A  680
GRVER2.SEQ   T C C G C T T G A T T C A T G C C C T G G A C C C A C G T G T G G G T A C T C A  680
GRVER1.SEQ   T C C G C T T G A T T C A T G C C C T G G A C C C A C G T G T G G G T A C C C A  680
YG81-6G1.SEQ T C C G A C T T A T A C A T G C T T T A G A C C C C A G G G C A G G A A C G C A  680
RDVER1.SEQ   T G C G T C T G A T C C A C G C T C T C G A T C C T C G C T A C G G C A C T C A  680
RDVER2.SEQ   T G C G T C T G A T C C A C G C T C T C G A T C C T C G C T A C G G C A C C C A  680
RDVER3.SEQ   T G C G T C T G A T C C A T G C T C T C G A T C C A C G C T A C G G C A C T C A  680
RDVER4.SEQ   T G C G T C T G A T C C A T G C T C T C G A T C C A C G C T A C G G C A C T C A  680
RDVER5.SEQ   T G C G T C T G A T C C A T G C T C T C G A T C C A C G C T A C G G C A C T C A  680
RD7.SEQ      T G C G T C T G A T C C A T G C T C T C G A T C C A C G C T A C G G C A C T C A  680
RDVER51.SEQ  T G C G T C T G A T C C A T G C T C T C G A T C C A C G C T A C G G C A C T C A  680
RDVER52.SEQ  T G C G T C T G A T C C A T G C T C T C G A T C C A C G C T A C G G C A C T C A  680
RD1561H9.SEQ T G C G T C T G A T C C A T G C T C T C G A T C C A C G C T A C G G C A C T C A  680

GRVER51.SEQ  A T T G A T C C C T G G C G T G A C T G T G C T G G T G T A T C T G C C T T T C  720
GR6.SEQ      A T T G A T C T C T G G C G T G A C T G T G C T G G T G T A T C T G C C T T T C  720
GRVER5.SEQ   A T T G A T C C C T G G C G T G A C T G T G C T G G T G T A T C T G C C T T T C  720
GRVER4.SEQ   A T T G A T C C C T G G C G T G A C T G T G C T G G T G T A T T T G C C T T T C  720
GRVER3.SEQ   A T T G A T C C C T G G C G T G A C T G T G C T G G T G T A C T T G C C A T T C  720
GRVER2.SEQ   G T T G A T C C C T G G C G T G A C T G T C C T G G T G T A C T T G C C A T T C  720
GRVER1.SEQ   G T T G A T C C C T G G C G T G A C T G T C C T G G T G T A C T T G C C A T T C  720
YG81-6G1.SEQ A C T T A T T C C T G G T G T G A C A G T C T T A G T A T A T C T G C C T T T T  720
RDVER1.SEQ   A C T G A T T C C A G G T G T C A C C G T G T T G G T C T A T C T G C C T T T T  720
RDVER2.SEQ   A C T G A T T C C T G G T G T C A C C G T G T T G G T C T A T C T G C C T T T T  720
RDVER3.SEQ   G C T G A T T C C T G G T G T C A C C G T C T T G G T C T A C C T G C C T T T C  720
RDVER4.SEQ   G C T G A T T C C T G G T G T C A C C G T C T T G G T C T A C T T G C C T T T C  720
RDVER5.SEQ   G C T G A T T C C T G G T G T C A C C G T C T T G G T C T A C T T G C C T T T C  720
RD7.SEQ      G C T G A T T C C T G G T G T C A C C G T C T T G G T C T A C T T G C C T T T C  720
RDVER51.SEQ  G C T G A T T C C T G G T G T C A C C G T C T T G G T C T A C T T G C C T T T C  720
RDVER52.SEQ  G C T G A T T C C T G G T G T C A C C G T C T T G G T C T A C T T G C C T T T C  720
RD1561H9.SEQ G C T G A T T C C T G G T G T C A C C G T C T T G G T C T A C T T G C C T T T C  720
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Figure 2 (cont.)

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GRVER51.SEQ   T T T C A C G C ● T T G G T T T C T C T A T T A C C ● G G C T A T T T C A 760
GR6.SEQ       T T T C A C G C C T T T G G T T T C T C T A T T A C C C T G G G C T A T T T C A 760
GRVER5.SEQ    T T T C A C G C C T T T G G T T T C T C T A T T A C C C T G G G C T A T T T C A 760
GRVER4.SEQ    T T T C A C G C C T T T G G T T T T T C T A T T A C C C T G G G C T A T T T C A 760
GRVER3.SEQ    T T T C A C G C C T T T G G T T T T T C T A T C A C C C T G G G C T A T T T C A 760
GRVER2.SEQ    T T T C A C G C C T T C G G T T T T T C T A T T A C C C T G G G C T A T T T C A 760
GRVER1.SEQ    T T T C A C G C C T T C G G T T T T T C T A T T A C C C T G G G C T A T T T C A 760
YG81-6G1.SEQ  T T C C A T G C T T T T G G G T T C T C T A T A A C C T T G G G A T A C T T C A 760
RDVER1.SEQ    T T C C A T G C T T T T G G C T T C C A C A T C A C T T T G G G T T A C T T T A 760
RDVER2.SEQ    T T C C A T G C T T T T G G C T T C C A C A T C A C T T T G G G T T A C T T T A 760
RDVER3.SEQ    T T C C A T G C T T T T C G G C T T C C A C A T A C T T T G G G T T A C T T T A 760
RDVER4.SEQ    T T C C A T G C T T T T C G G C T T C C A T A T T A C T T T G G G T T A C T T T A 760
RDVER5.SEQ    T T C C A T G C T T T T C G G C T T T C A T A T T A C T T T G G G T T A C T T T A 760
RD7.SEQ       T T C C A T G C T T T T C G G C T T T C A T A T T A C T T T G G G T T A C T T T A 760
RDVER51.SEQ   T T C C A T G C T T T T C G G C T T T C A T A T T A C T T T G G G T T A C T T T A 760
RDVER52.SEQ   T T C C A T G C T T T T C G G C T T T C A T A T T A C T T T G G G T T A C T T T A 760
RD1561H9.SEQ  T T C C A T G C T T T T C G G C T T T C A T A T T A C T T T G G G T T A C T T T A 760

GRVER51.SEQ   T G G T C G G C T T G C G T G T C A T C A T G T T T C G T C G C T T C G A C C A 800
GR6.SEQ       T G G T C G G C T T G C G T G T C A T C A T G T T T C G T C G C T T C G A C C A 800
GRVER5.SEQ    T G G T C G G C T T G C G T G T C A T C A T G T T T C G T C G C T T C G A C C A 800
GRVER4.SEQ    T G G T C G G C T T G C G T G T C A T C A T G T T T C G T C G C T T C G A C C A 800
GRVER3.SEQ    T G G T C G G C T T G C G T G T G A T C A T G T T T C G T C G C T T C G A C C A 800
GRVER2.SEQ    T G G T C G G T T T G C G C G T G A T C A T G T T T C G T C G C T T C G A T C A 800
GRVER1.SEQ    T G G T C G G T T T G C G C G T G A T C A T G T T T C G T C G C T T C G A T C A 800
YG81-6G1.SEQ  T G G T G G G T C T T C G T G T T A T C A T G T T C A G A C G A T T T G A T C A 800
RDVER1.SEQ    T G G T G G G C C T G C G T G T C A T T A T G T T C C G C C G T T T T G A C C A 800
RDVER2.SEQ    T G G T G G G C C T G C G T G T C A T T A T G T T C C G C C G T T T T G A C C A 800
RDVER3.SEQ    T G G T C G G T C T G C G T G T C A T T A T G T T C C G C C G T T T T G A T C A 800
RDVER4.SEQ    T G G T C G G T C T G C G T G T G A T T A T G T T C C G C C G T T T T G A T C A 800
RDVER5.SEQ    T G G T C G G T C T C C G C G T G A T T A T G T T C C G C C G T T T T G A T C A 800
RD7.SEQ       T G G T C G G T C T C C G C G T G A T T A T G T T C C G C C G T T T T G A T C A 800
RDVER51.SEQ   T G G T C G G T C T C C G C G T G A T T A T G T T C C G C C G T T T T G A T C A 800
RDVER52.SEQ   T G G T C G G T C T C C G C G T G A T T A T G T T C C G C C G T T T T G A T C A 800
RD1561H9.SEQ  T G G T C G G T C T C C G C G T G A T T A T G T T C C G C C G T T T T G A T C A 800

GRVER51.SEQ   A G A A G C C T T C T T G A A G G C T A T T C A A G A C T A C G A G G T G C G T 840
GR6.SEQ       A G A A G C C T T C T T G A A G G C T A T T C A A G A C T A C G A G G T G C G T 840
GRVER5.SEQ    A G A A G C C T T C T T G A A G G C T A T T C A A G A C T A C G A G G T G C G T 840
GRVER4.SEQ    A G A A G C C T T C T T G A A G G C T A T T C A A G A C T A C G A G G T G C G T 840
GRVER3.SEQ    A G A A G C C T T C C T G A A G G C T A T T C A A G A C T A C G A G G T G C G T 840
GRVER2.SEQ    A G A A G C C T T T C T G A A G G C C A T T C A A G A C T A C G A G G T C C G T 840
GRVER1.SEQ    A G A A G C T T T T C T G A A G G C C A T T C A G G A C T A C G A G G T C C G T 840
YG81-6G1.SEQ  A G A A G C A T T T C T A A A A G C T A T T C A G G A T T A T G A A G T T C G A 840
RDVER1.SEQ    G G A G G C C T T C T T G A A A G C T A T C C A A G A T T A T G A A G T G C G C 840
RDVER2.SEQ    G G A G G C T T T C T T G A A A G C T A T C C A A G A T T A T G A A G T G C G C 840
RDVER3.SEQ    G G A G G C T T T T T T G A A A G C C A T C C A A G A T T A T G A A G T C C G C 840
RDVER4.SEQ    G G A G G C T T T C T T G A A A G C C A T C C A A G A T T A T G A A G T C C G C 840
RDVER5.SEQ    G G A G G C T T T C T T G A A A G C C A T C C A A G A T T A T G A A G T C C G C 840
RD7.SEQ       G G A G G C T T T C T T G A A A G C C A T C C A A G A T T A T G A A G T C C G C 840
RDVER51.SEQ   G G A G G C T T T C T T G A A A G C C A T C C A A G A T T A T G A A G T C C G C 840
RDVER52.SEQ   G G A G G C T T T C T T G A A A G C C A T C C A A G A T T A T G A A G T C C G C 840
RD1561H9.SEQ  G G A G G C T T T C T T G A A A G C C A T C C A A G A T T A T G A A G T C C G C 840
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Figure 2 (cont.)

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GRVER51.SEQ   T C C G T G A T C A C G T C C C T T C A G T C A T T T T T C C T G A G C A   880
GR6.SEQ       T C C G T G A T C A A C G T C C C T T C A G T C A T T T T G T T C C T G A G C A   880
GRVER5.SEQ    T C C G T G A T C A A C G T C C C T T C A G T C A T T T T G T T C C T G A G C A   880
GRVER4.SEQ    T C T G T C A T C A A T G T C C C T T C A G T C A T T T T G T T C C T G A G C A   880
GRVER3.SEQ    T C T G T G A T C A A T G T C C C A T C T G T C A T T T T G T T C C T G A G C A   880
GRVER2.SEQ    A G C G T G A T C A A C G T C C C T T C T G T G A T T T T T G T T C C T G A G C A   880
GRVER1.SEQ    A G C G T G A T C A A C G T C C C T T C T G T G A T T T T T G T T C C T G A G C A   880
YG81-6G1.SEQ  A G T G T A A T T A A C G T T C C A T C A G T A A T A T T G T T C T T A T C G A   880
RDVER1.SEQ    T C T G T C A T T A A T G T G C C A A G C G T C A T C C T G T T T T T G T C T A   880
RDVER2.SEQ    T C T G T C A T T A A T G T G C C A A G C G T C A T C C T G T T T T T G T C T A   880
RDVER3.SEQ    A G C G T C A T T A A C G T G C C T A G C G T G A T C C T G T T T T T G T C T A   880
RDVER4.SEQ    A G T G T C A T C A A C G T G C C T A G C G T G A T C C T G T T T T T G T C T A   880
RDVER5.SEQ    A G T G T C A T C A A C G T G C C T A G C G T G A T C C T G T T T T T G T C T A   880
RD7.SEQ       A G T G T C A T C A A C G T G C C T A G C G T G A T C C T G T T T T T G T C T A   880
RDVER51.SEQ   A G T G T C A T C A A C G T G C C T A G C G T G A T C C T G T T T T T G T C T A   880
RDVER52.SEQ   A G T G T C A T C A A C G T G C C T A G C G T G A T C C T G T T T T T G T C T A   880
RD1561H9.SEQ  A G T G T C A T C A A C G T G C C T A G C G T G A T C C T G T T T T T G T C T A   880


GRVER51.SEQ   A A T C T C C T T T G G T T G A C A A G T A T G A T C T G A G C A G C T T G C G   920
GR6.SEQ       A A T C T C C T T T G G T T G A C A A G T A T G A T C T G A G C A G C T T G C G   920
GRVER5.SEQ    A A T C T C C T T T G G T T G A C A A G T A T G A T C T G A G C A G C T T G C G   920
GRVER4.SEQ    A A T C T C C T T T G G T T G A C A A G T A T G A T C T G A G C A G C T T G C G   920
GRVER3.SEQ    A A T C T C C T T T G G T T G A C A A G T A T G A T C T G A G C A G C T T G C G   920
GRVER2.SEQ    A A T C T C C A T T G G T C G A T A A G T A T G A C C T G A G C A G C T T G C G   920
GRVER1.SEQ    A A T C T C C A T T G G T C G A T A A G T A T G A C C T G A G C T C T T T G C G   920
YG81-6G1.SEQ  A A A G T C C T T T G G T T G A C A A A T A C G A T T T A T C A A G T T T A A G   920
RDVER1.SEQ    A G A G C C C T C T G G T G G A C A A A T A C G A T T T G T C T A G C C T G C G   920
RDVER2.SEQ    A G A G C C C T C T G G T G G A C A A A T A C G A T T T G T C T T C T C T G C G   920
RDVER3.SEQ    A G A G C C C A C T C G T G G A C A A G T A C G A C T T G T C T T C C C T G C G   920
RDVER4.SEQ    A G A G C C C A C T C G T G G A C A A G T A C G A C T T G T C T T C A C T G C G   920
RDVER5.SEQ    A G A G C C C A C T C G T G G A C A A G T A C G A C T T G T C T T C A C T G C G   920
RD7.SEQ       A G A G C C C A C T C G T G G A C A A G T A C G A C T T G T C T T C A C T G C G   920
RDVER51.SEQ   A G A G C C C A C T C G T G G A C A A G T A C G A C T T G T C T T C A C T G C G   920
RDVER52.SEQ   A G A G C C C A C T C G T G G A C A A G T A C G A C T T G T C T T C A C T G C G   920
RD1561H9.SEQ  A G A G C C C A C T C G T G G A C A A G T A C G A C T T G T C T T C A C T G C G   920


GRVER51.SEQ   T G A G C T G T G C T G T G G C G C T G C T C C T T T G G C C A A A G A A G T G   960
GR6.SEQ       T G A G C T G T G C T G T G G C G C T G C T C C T T T G G C C A A A G A A G T G   960
GRVER5.SEQ    T G A G C T G T G C T G T G G C G C T G C T C C T T T G G C C A A A G A A G T G   960
GRVER4.SEQ    T G A G C T G T G C T G T G G C G C T G C T C C T T T G G C C A A A G A A G T G   960
GRVER3.SEQ    T G A A C T G T G C T G T G G C G C T G C T C C T T T G G C C A A A G A A G T G   960
GRVER2.SEQ    C G A A C T G T G C T G T G G C G C T G C C C C T T T G G C T A A A G A G G T G   960
GRVER1.SEQ    C G A A C T G T G C T G T G G C G C T G C C C C T T T G G C T A A A G A G G T G   960
YG81-6G1.SEQ  G G A A T T G T G T T G C G G T G C G G C A C C A T T A G C A A A A G A A G T T   960
RDVER1.SEQ    T G A G T T G T G T T G C G G T G C C G C T C C A C T G G C C A A G G A A G T C   960
RDVER2.SEQ    T G A G T T G T G T T G C G G T G C C G C T C C A C T G G C C A A G G A A G T C   960
RDVER3.SEQ    T G A G T T G T G T T G C G G T G C C G C C C C A C T G G C T A A G G A G G T C   960
RDVER4.SEQ    T G A A T T G T G T T G C G G T G C C G C T C C A C T G G C T A A G G A G G T C   960
RDVER5.SEQ    T G A A T T G T G T T G C G G T G C C G C T C C A C T G G C T A A G G A G G T C   960
RD7.SEQ       T G A A T T G T G T T G C G G T G C C G C T C C A C T G G C T A A G G A G G T C   960
RDVER51.SEQ   T G A A T T G T G T T G C G G T G C C G C T C C A C T G G C T A A G G A G G T C   960
RDVER52.SEQ   T G A A T T G T G T T G C G G T G C C G C T C C A C T G G C T A A G G A G G T C   960
RD1561H9.SEQ  T G A A T T G T G T T G C G G T G C C G C T C C A C T G G C T A A G G A G G T C   960
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Figure 2 (cont.)

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GRVER51.SEQ  G C C G A G G T C G C T G C T A A G C G T C T G A A C C ● C C T G G T A T C C  1000
GR6.SEQ      G C C G A G G T C G C T G C T A A G C G T C T G A A C C T C C C T G G T A T C C  1000
GRVER5.SEQ   G C C G A G G T C G C T G C T A A G C G T C T G A A C C T C C C T G G T A T C C  1000
GRVER4.SEQ   G C C G A G G T C G C T G C T A A G C G T C T G A A C C T C C C T G G T A T C C  1000
GRVER3.SEQ   G C C G A G G T C G C T G C T A A G C G T C T G A A C C T C C C T G G T A T C C  1000
GRVER2.SEQ   G C C G A A G T C G C T G C C A A G C G T C T G A A T T T G C C A G G T A T C C  1000
GRVER1.SEQ   G C C G A A G T C G C T G C C A A G C G T C T G A A T T T G C C A G G T A T C C  1000
YG81-6G1.SEQ G C T G A G G T T G C A G C A A A A C G A T T A A A C T T G C C A G G A A T T C  1000
RDVER1.SEQ   G C T G A G G T G G C C G C T A A A C G C T T G A A C C T G C C T G G C A T T C  1000
RDVER2.SEQ   G C T G A G G T G G C C G C T A A A C G C T T G A A C C T G C C T G G C A T T C  1000
RDVER3.SEQ   G C T G A A G T G G C C G C C A A A C G C T T G A A T C T G C C A G G C A T T C  1000
RDVER4.SEQ   G C T G A A G T G G C C G C C A A A C G C T T G A A T C T G C C C G G C A T T C  1000
RDVER5.SEQ   G C T G A A G T G G C C G C C A A A C G C T T G A A T C T T C C A G G G A T T C  1000
RD7.SEQ      G C T G A A G T G G C C G C C A A A C G C T T G A A T C T T C C A G G G A T T C  1000
RDVER51.SEQ  G C T G A A G T G G C C G C C A A A C G C T T G A A T C T T C C A G G G A T T C  1000
RDVER52.SEQ  G C T G A A G T G G C C G C C A A A C G C T T G A A T C T T C C A G G G A T T C  1000
RD1561H9.SEQ G C T G A A G T G G C C C G C C A A A C G C T T G A A T C T T C C A G G G A T T C  1000


GRVER51.SEQ  G C T G C G G T T T T G G T T T G A C T G A G A G C A C T T C T G C T A A C A T  1040
GR6.SEQ      G C T G C G G T T T T G G T T T G A C T G A G A G C A C T T C T G C T A A C A T  1040
GRVER5.SEQ   G C T G C G G T T T T G G T T T G A C T G A G A G C A C T T C T G C T A A C A T  1040
GRVER4.SEQ   G C T G C G G T T T T G G T T T G A C T G A G A G C A C T T C T G C T A A C A T  1040
GRVER3.SEQ   G C T G C G G T T T T G G T T T G A C T G A G A G C A C T T C T G C C A A C A T  1040
GRVER2.SEQ   G C T G C G G C T T T G G T C T G A C T G A G A G C A C C T C T G C T A A C A T  1040
GRVER1.SEQ   G C T G C G G C T T T G G T C T G A C T G A G A G C A C C T C T G C T A A C A T  1040
YG81-6G1.SEQ G C T G T G G A T T T G G T T T G A C A G A A T C T A C T T C A G C T A A T A T  1040
RDVER1.SEQ   G T T G T G G T T T C G G C T T G A C C G A A T C T A C T A G C G C C A T T A T  1040
RDVER2.SEQ   G T T G T G G T T T C G G C T T G A C C G A A T C T A C T A G C G C C A T T A T  1040
RDVER3.SEQ   G T T G T G G C T T C G G C C T C A C C G A A T C T A C C A G C G C T A T T A T  1040
RDVER4.SEQ   G T T G T G G C T T C G G C C T C A C C G A A T C T A C C A G C G C T A T T A T  1040
RDVER5.SEQ   G T T G T G G C T T C G G C C T C A C C G A A T C T A C C A G C G C T A T T A T  1040
RD7.SEQ      G T T G T G G C T T C G G C C T C A C C G A A T C T A C C A G C G C T A T T A T  1040
RDVER51.SEQ  G T T G T G G C T T C G G C C T C A C C G A A T C T A C C A G C G C T A T T A T  1040
RDVER52.SEQ  G T T G T G G C T T C G G C C T C A C C G A A T C T A C C A G C G C T A T T A T  1040
RD1561H9.SEQ G T T G T G G C T T C G G C C T C A C C G A A T C T A C C A G T G C G A T T A T  1040


GRVER51.SEQ  C C A T A G C T T G C G A G A C G A G T T T A A G T C T G G T A G C C T G G G T  1080
GR6.SEQ      C C A T A G C T T G C G A G A C G A G T T T A A G T C T G G T A G C C T G G G T  1080
GRVER5.SEQ   C C A T A G C T T G C G A G A C G A G T T T A A G T C T G G T A G C C T G G G T  1080
GRVER4.SEQ   C C A T A G C T T G C G A G A C G A G T T T A A G T C T G G T A G C C T G G G T  1080
GRVER3.SEQ   C C A T A G C T T G C G T G A C G A G T T T A A A T C T G G T A G C C T G G G T  1080
GRVER2.SEQ   T C A T A G C T T G C G T G A T G A G T T C A A A T C T G G C A G C C T G G G T  1080
GRVER1.SEQ   T C A T A G C T T G C G T G A T G A A T T C A A A T C T G G C A G C C T G G G T  1080
YG81-6G1.SEQ A C A C A G T C T T A G G G A T G A A T T T A A A T C A G G A T C A C T T G G A  1080
RDVER1.SEQ   C C A A T C T C T G C G C G A C G A G T T T A A G A G C G G T T C T T T G G G C  1080
RDVER2.SEQ   C C A A T C T C T G C G C G A C G A A T T T A A G A G C G G T T C T T T G G G C  1080
RDVER3.SEQ   T C A A T C T C T C C G C G A T G A G T T T A A G A G C G G C T C T T T G G G C  1080
RDVER4.SEQ   T C A G T C T C T C C G C G A T G A G T T T A A G A G C G G C T C T T T G G G C  1080
RDVER5.SEQ   T C A G T C T C T C C G C G A T G A G T T T A A G A G C G G C T C T T T G G G C  1080
RD7.SEQ      T C A G T C T C T C C G C G A T G A G T T T A A G A G C G G C T C T T T G G G C  1080
RDVER51.SEQ  T C A G T C T C T C C G C G A T G A G T T T A A G A G C G G C T C T T T G G G C  1080
RDVER52.SEQ  T C A G T C T C T C G G G G A T G A G T T T A A G A G C G G C T C T T T G G G C  1080
RD1561H9.SEQ C C A G A C T C T C G G G G A T G A G T T T A A G A G C G G C T C T T T G G G C  1080
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Figure 2 (Cont.)

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GRVER51.SEQ   C G C G T G A C ●   T C T T A T G G C T G C A A A G A ● G C C G A C C G T G   1120
GR6.SEQ       C G C G T G A C T C C T C T T A T G G C T G C A A A G A T C G C C G A C C G T G   1120
GRVER5.SEQ    C G C G T G A C T C C T C T T A T G G C T G C A A A G A T C G C C G A C C G T G   1120
GRVER4.SEQ    C G C G T G A C T C C T C T T A T G G C T G C A A A G A T C G C C G A C C G T G   1120
GRVER3.SEQ    C G C G T G A C C C C T T T G A T G G C T G C A A A G A T C G C C G A C C G T G   1120
GRVER2.SEQ    C G C G T G A C T C C T T T G A T G G C C G C T A A G A T C G C C G A C C G T G   1120
GRVER1.SEQ    C G C G T G A C T C C T T T G A T G G C C G C T A A G A T C G C C G A C C G T G   1120
YG81-6G1.SEQ  A G A G T T A C T C C T T T A A T G G C A G C T A A A A T A G C A G A T A G G G   1120
RDVER1.SEQ    C G T G T C A C C C C A C T G A T G G C T G C C A A A A T T G C T G A T C G C C G   1120
RDVER2.SEQ    C G T G T C A C C C C A C T G A T G G C T G C C A A A A T T G C T G A T C G C C G   1120
RDVER3.SEQ    C G T G T C A C T C C A C T C A T G G C T G C T A A A A T C G C T G A T C G C C G   1120
RDVER4.SEQ    C G T G T C A C T C C A C T C A T G G C T G C T A A G A T C G C T G A T C G C C G   1120
RDVER5.SEQ    C G T G T C A C T C C A C T C A T G G C T G C T A A G A T C G C T G A T C G C C G   1120
RD7.SEQ       C G T G T C A C T C C A C T C A T G G C T G C T A A G A T C G C T G A T C G C C G   1120
RDVER51.SEQ   C G T G T C A C T C C A C T C A T G G C T G C T A A G A T C G C T G A T C G C C G   1120
RDVER52.SEQ   C G T G T C A C T C C A C T C A T G G C T G C T A A G A T C G C T G A T C G C C G   1120
RD1561H9.SEQ  C G T G T C A C T C C A C T C A T G G C T G C T A A G A T C G C T G A T C G C C G   1120


GRVER51.SEQ   A G A C C G G C A A A G C A C T G G G C C C A A A T C A A G T C G G T G A A T T   1160
GR6.SEQ       A G A C C G G C A A A G C A C T G G G C C C A A A T C A A G T C G G T G A A T T   1160
GRVER5.SEQ    A G A C C G G C A A A G C A C T G G G C C C A A A T C A A G T C G G T G A A T T   1160
GRVER4.SEQ    A G A C C G G C A A A G C A C T G G G C C C A A A T C A A G T C G G T G A A T T   1160
GRVER3.SEQ    A G A C C G G C A A A G C C C T G G G C C C A A A T C A G G T C G G T G A A T T   1160
GRVER2.SEQ    A G A C C G G C A A A G C T C T G G G T C C A A A T C A A G T C G G C G A A T T   1160
GRVER1.SEQ    A G A C C G G C A A A G C T C T G G G T C C A A A T C A A G T C G G C G A A T T   1160
YG81-6G1.SEQ  A A A C T G G T A A A G C A T T G G G A C C A A A T C A A G T T G G T G A A T T   1160
RDVER1.SEQ    A A A C T G G T A A G G C C T T G G G C C C T A A C C A G G T G G G T G A G C T   1160
RDVER2.SEQ    A A A C T G G T A A G G C C T T G G G C C C T A A C C A G G T G G G T G A G C T   1160
RDVER3.SEQ    A A A C T G G T A A G G C T T T G G G C C C T A A C C A A G T G G G C G A G C T   1160
RDVER4.SEQ    A A A C T G G T A A G G C T T T G G G C C C T A A C C A A G T G G G C G A G C T   1160
RDVER5.SEQ    A A A C T G G T A A G G C T T T G G G C C C T A A C C A A G T G G G C G A G C T   1160
RD7.SEQ       A A A C T G G T A A G G C T T T G G G C C C G A A C C A A G T G G G C G A G C T   1160
RDVER51.SEQ   A A A C T G G T A A G G C T T T G G G C C C G A A C C A A G T G G G C G A G C T   1160
RDVER52.SEQ   A A A C T G G T A A G G C T T T G G G C C C G A A C C A A G T G G G C G A G C T   1160
RD1561H9.SEQ  A A A C T G G T A A G G C T T T G G G C C C G A A C C A A G T G G G C G A G C T   1160


GRVER51.SEQ   G T G T A T T A A G G G C C C T A T G G T C T C T A A A G G C T A C G T G A A C   1200
GR6.SEQ       G T G T A T T A A G G G C C C T A T G G T C T C T A A A G G C T A C G T G A A C   1200
GRVER5.SEQ    G T G T A T T A A G G G C C C T A T G G T C T C T A A A G G C T A C G T G A A C   1200
GRVER4.SEQ    G T G T A T T A A G G G C C C T A T G G T C T C T A A A G G C T A C G T G A A C   1200
GRVER3.SEQ    G T G C A T T A A G G G C C C T A T G G T C T C T A A A G G C T A C G T G A A C   1200
GRVER2.SEQ    G T G T A T T A A G G G T C C T A T G G T G T C T A A A G G C T A C G T C A A C   1200
GRVER1.SEQ    G T G T A T T A A G G G T C C T A T G G T G T C T A A A G G C T A C G T C A A C   1200
YG81-6G1.SEQ  A T G C A T T A A A G G T C C C A T G G T A T C G A A A G G T T A C G T G A A C   1200
RDVER1.SEQ    G T G C A T C A A A G G C C C A A T G G T C A G C A A G G G T T A T G T G A A T   1200
RDVER2.SEQ    G T G C A T C A A A G G C C C A A T G G T C A G C A A G G G T T A T G T G A A T   1200
RDVER3.SEQ    G T G T A T C A A A G G C C C T A T G G T G A G C A A G G G T T A T G T C A A T   1200
RDVER4.SEQ    G T G T A T C A A A G G C C C T A T G G T G A G C A A G G G T T A T G T C A A T   1200
RDVER5.SEQ    G T G T A T C A A A G G C C C T A T G G T G A G C A A G G G T T A T G T C A A T   1200
RD7.SEQ       G T G T A T C A A A G G C C C T A T G G T G A G C A A G G G T T A T G T C A A T   1200
RDVER51.SEQ   G T G T A T C A A A G G C C C T A T G G T G A G C A A G G G T T A T G T C A A T   1200
RDVER52.SEQ   G T G T A T C A A A G G C C C T A T G G T G A G C A A G G G T T A T G T C A A T   1200
RD1561H9.SEQ  G T G T A T C A A A G G C C C T A T G G T G A G C A A G G G T T A T G T C A A T   1200
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Figure 2 (cont.)

```
GRVER51.SEQ  A A T G T G G A ● C C A C T A A A G A A G C C A T T ● G A T G A T G G C T  1240
GR6.SEQ      A A T G T G G A G G C C A C T A A A G A A G C C A T T G A T G A T G A T G G C T  1240
GRVER5.SEQ   A A T G T G G A G G C C A C T A A A G A A G C C A T T G A T G A T G A T G G C T  1240
GRVER4.SEQ   A A T G T G G A G G C C A C T A A A G A A G C C A T T G A T G A T G A T G G C T  1240
GRVER3.SEQ   A A T G T G G A G G C C A C T A A A G A A G C T A T T G A T G A T G A T G G T T  1240
GRVER2.SEQ   A A T G T G G A G G C C A C T A A G G A A G C T A T T G A T G A C G A T G G T T  1240
GRVER1.SEQ   A A T G T G G A G G C C A C T A A G G A A G C T A T C G A T G A C G A T G G T T  1240
YG81-6G1.SEQ A A T G T A G A A G C T A C C A A A G A A G C T A T T G A T G A T G A T G G T T  1240
RDVER1.SEQ   A A C G T C G A A G C T A C C A A A G A G G C C A T T G A C G A T G A C G G C T  1240
RDVER2.SEQ   A A C G T C G A A G C T A C C A A A G A G G C C A T C G A C G A T G A C G G C T  1240
RDVER3.SEQ   A A C G T C G A A G C T A C C A A G G A G G C C A T C G A C G A C G A C G G C T  1240
RDVER4.SEQ   A A C G T C G A A G C T A C C A A G G A G G C T A T C G A C G A C G A C G G C T  1240
RDVER5.SEQ   A A C G T C G A A G C T A C C A A G G A G G C C A T C G A C G A C G A C G G C T  1240
RD7.SEQ      A A C G T T G A A G C T A C C A A G G A G G C C A T C G A C G A C G A C G G C T  1240
RDVER51.SEQ  A A C G T T G A A G C T A C C A A G G A G G C C A T C G A C G A C G A C G G C T  1240
RDVER52.SEQ  A A C G T T G A A G C T A C C A A G G A G G C C A T C G A C G A C G A C G G C T  1240
RD1561H9.SEQ A A C G T T G A A G C T A C C A A G G A G G C C A T C G A C G A C G A C G G C T  1240


GRVER51.SEQ  G G C T C C A T A G C G G C G A C T T C G G T T A C T A T G A T G A G G A C G A  1280
GR6.SEQ      G G C T C C A T A G C G G C G A C T T C G G T T A C T A T G A T G A G G A C G A  1280
GRVER5.SEQ   G G C T C C A T A G C G G C G A C T T C G G T T A C T A T G A T G A G G A C G A  1280
GRVER4.SEQ   G G C T C C A T A G C G G C G A C T T C G G T T A C T A T G A T G A G G A C G A  1280
GRVER3.SEQ   G G T T G C A T A G C G G C G A C T T C G G T T A T T A T G A T G A G G A C G A  1280
GRVER2.SEQ   G G C T G C A C A G C G G C G A C T T T G G T T A T T A C G A T G A G G A C G A  1280
GRVER1.SEQ   G G C T G C A C A G C G G C G A C T T T G G T T A T T A C G A T G A G G A C G A  1280
YG81-6G1.SEQ G G C T T C A C T C T G G A G A C T T T G G A T A C T A T G A T G A G G A T G A  1280
RDVER1.SEQ   G G T T G C A T T C T G G T G A T T T C G G C T A C T A T G A C G A A G A T G A  1280
RDVER2.SEQ   G G T T G C A T T C T G G T G A T T T C G G C T A C T A T G A C G A A G A T G A  1280
RDVER3.SEQ   G G C T G C A T T C T G G T G A T T T T G G C T A C T A C G A C G A A G A T G A  1280
RDVER4.SEQ   G G T T G C A T T C T G G T G A T T T T G G A T A T T A C G A C G A A G A T G A  1280
RDVER5.SEQ   G G T T G C A T T C T G G T G A T T T T G G A T A T T A C G A C G A A G A T G A  1280
RD7.SEQ      G G T T G C A T T C T G G T G A T T T T G G A T A T T A C G A C G A A G A T G A  1280
RDVER51.SEQ  G G T T G C A T T C T G G T G A T T T T G G A T A T T A C G A C G A A G A T G A  1280
RDVER52.SEQ  G G T T G C A T T C T G G T G A T T T T G G A T A T T A C G A C G A A G A T G A  1280
RD1561H9.SEQ G G T T G C A T T C T G G T G A T T T T G G A T A T T A C G A C G A A G A T G A  1280


GRVER51.SEQ  A C A C T T C T A T G T G G T C G A T C G C T A C A A A G A A T T G A T T A A G  1320
GR6.SEQ      A C A C T T C T A T G T G G T C G A T C G C T A C A A A G A A T T G A T T A A G  1320
GRVER5.SEQ   A C A C T T C T A T G T G G T C G A T C G C T A C A A A G A A T T G A T T A A G  1320
GRVER4.SEQ   A C A C T T C T A T G T G G T C G A T C G C T A C A A A G A A T T G A T T A A G  1320
GRVER3.SEQ   A C A C T T C T A T G T G G T C G A T C G C T A T A A A G A A T T G A T T A A G  1320
GRVER2.SEQ   A C A T T T C T A T G T C G T C G A T C G C T A C A A A G A G T T G A T T A A G  1320
GRVER1.SEQ   A C A T T T C T A T G T C G T G G A T C G C T A C A A A G A G T T G A T T A A G  1320
YG81-6G1.SEQ G C A T T T C T A T G T G G T G G A C C G T T A C A A G G A A T T G A T T A A A  1320
RDVER1.SEQ   G C A C T T T T A C G T G G T C G A C C G T T A T A A G G A A C T G A T C A A A  1320
RDVER2.SEQ   G C A C T T T T A C G T G G T G G A C C G T T A T A A G G A A C T G A T C A A A  1320
RDVER3.SEQ   G C A T T T T T A C G T C G T G G A T C G T T A C A A G G A G C T G A T C A A A  1320
RDVER4.SEQ   G C A T T T T T A C G T C G T G G A T C G T T A C A A G G A G C T G A T C A A A  1320
RDVER5.SEQ   G C A T T T T T A C G T C G T G G A T C G T T A C A A G G A G C T G A T C A A A  1320
RD7.SEQ      G C A T T T T T A C G T C G T G G A T C G T T A C A A G G A G C T G A T C A A A  1320
RDVER51.SEQ  G C A T T T T T A C G T C G T G G A T C G T T A C A A G G A G C T G A T C A A A  1320
RDVER52.SEQ  G C A T T T T T A C G T C G T G G A T C G T T A C A A G G A G C T G A T C A A A  1320
RD1561H9.SEQ G C A T T T T T A C G T C G T G G A T C G T T A C A A G G A G C T G A T C A A A  1320
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Figure 2 (cont.)

```
GRVER51.SEQ  T A C A A A G G ●   C T C A A G T C G C A C C A G C C G ●   C T G G A A G A A A  1360
GR6.SEQ      T A C A A A G G C T C T C A A G T C G C A C C A G C C G A A C T G G A A G A A A  1360
GRVER5.SEQ   T A C A A A G G C T C T C A A G T C G C A C C A G C C G A A C T G G A A G A A A  1360
GRVER4.SEQ   T A C A A A G G C T C T C A A G T C G C C C C A G C C G A A C T G G A A G A A A  1360
GRVER3.SEQ   T A C A A A G G C T C T C A A G T C G C C C C A G C T G A A C T G G A A G A A A  1360
GRVER2.SEQ   T A T A A A G G C T C T C A A G T C G C C C C A G C T G A G C T G G A A G A A A  1360
GRVER1.SEQ   T A T A A A G G C T C T C A G G T C G C C C C A G C T G A G C T G G A A G A G A  1360
YG81-6G1.SEQ T A T A A G G G C T C T C A G G T A G C A C C T G C A G A A C T A G A A G A G A  1360
RDVER1.SEQ   T A C A A G G G T A G C C A A G T G G C T C C T G C C G A A T T G G A G G A A A  1360
RDVER2.SEQ   T A C A A G G G T A G C C A A G T G G C T C C T G C C G A A T T G G A G G A G A  1360
RDVER3.SEQ   T A C A A G G G T A G C C A G G T G G C T C C A G C C G A G T T G G A G G A G A  1360
RDVER4.SEQ   T A C A A G G G T A G C C A G G T T G C T C C A G C T G A G T T G G A G G A G A  1360
RDVER5.SEQ   T A C A A G G G T A G C C A G G T T G C T C C A G C T G A G T T G G A G G A G A  1360
RD7.SEQ      T A C A A G G G T A G C C A G G T T G C T C C A G C T G A G T T G G A G G A G A  1360
RDVER51.SEQ  T A C A A G G G T A G C C A G G T T G C T C C A G C T G A G T T G G A G G A G A  1360
RDVER52.SEQ  T A C A A G G G T A G C C A G G T T G C T C C A G C T G A G T T G G A G G A G A  1360
RD1561H9.SEQ T A C A A G G G T A G C C A G G T T G C T C C A G C T G A G T T G G A G G A G A  1360


GRVER51.SEQ  T T T T G C T G A A G A A C C C T T G T A T C C G C G A C G T G G C C G T C G T  1400
GR6.SEQ      T T T T G C T G A A G A A C C C T T G T A T C C G C G A C G T G G C C G T C G T  1400
GRVER5.SEQ   T T T T G C T G A A G A A C C C T T G T A T C C G C G A C G T G G C C G T C G T  1400
GRVER4.SEQ   T T T T G C T G A A G A A C C C T T G T A T C C G C G A C G T G G C C G T C G T  1400
GRVER3.SEQ   T T T T G C T G A A G A A C C C T T G T A T T C G C G A C G T G G C C G T C G T  1400
GRVER2.SEQ   T C T T G C T G A A G A A C C C T T G C A T T C G T G A C G T G G C C G T C G T  1400
GRVER1.SEQ   T C T T G C T G A A G A A C C C T T G C A T T C G T G A C G T G G C C G T C G T  1400
YG81-6G1.SEQ T T T T A T T G A A A A A T C C A T G T A T C A G A G A T G T T G C T G T G G T  1400
RDVER1.SEQ   T T C T G T T G A A A A A T C C A T G T A T C C G C G A T G T C G C T G T G G T  1400
RDVER2.SEQ   T T C T G T T G A A A A A T C C A T G T A T C C G C G A T G T C G C T G T G G T  1400
RDVER3.SEQ   T T C T G T T G A A A A A T C C A T G C A T C C G T G A T G T C G C T G T G G T  1400
RDVER4.SEQ   T T C T G T T G A A A A A T C C A T G C A T T C G C G A T G T C G C T G T G G T  1400
RDVER5.SEQ   T T C T G T T G A A A A A T C C A T G C A T T C G C G A T G T C G C T G T G G T  1400
RD7.SEQ      T T C T G T T G A A A A A T C C A T G C A T T C G C G A T G T C G C T G T G G T  1400
RDVER51.SEQ  T T C T G T T G A A A A A T C C A T G C A T T C G C G A T G T C G C T G T G G T  1400
RDVER52.SEQ  T T C T G T T G A A A A A T C C A T G C A T T C G C G A T G T C G C T G T G G T  1400
RD1561H9.SEQ T T C T G T T G A A A A A T C C A T G C A T T C G C G A T G T C G C T G T G G T  1400


GRVER51.SEQ  G G G T A T C C C A G A C T T G G A A G C T G G C G A G T T G C C T A G C G C C  1440
GR6.SEQ      G G G T A T C C C A G A C T T G G A A G C T G G C G A G T T G C C T A G C G C C  1440
GRVER5.SEQ   G G G T A T C C C A G A C T T G G A A G C T G G C G A G T T G C C T A G C G C C  1440
GRVER4.SEQ   G G G T A T C C C A G A C T T G G A A G C T G G T G A G T T G C C T A G C G C C  1440
GRVER3.SEQ   G G G T A T C C C A G A C T T G G A A G C T G G C G A G T T G C C T A G C G C C  1440
GRVER2.SEQ   G G G T A T C C C A G A T T T G G A A G C T G G C G A G C T G C C T A G C G C C  1440
GRVER1.SEQ   G G G T A T C C C A G A T T T G G A A G C T G G C G A G C T G C C T A G C G C C  1440
YG81-6G1.SEQ T G G T A T T C C T G A T C T A G A A G C T G G A G A A C T G C C A T C T G C G  1440
RDVER1.SEQ   C G G C A T T C C T G A C C T G G A G G C C G G T G A A T T G C C A T C T G C T  1440
RDVER2.SEQ   C G G C A T T C C T G A C C T G G A G G C C G G T G A A T T G C C A T C T G C T  1440
RDVER3.SEQ   C G G C A T T C C T G A T C T G G A G G C C G G T G A A C T G C C T T C T G C T  1440
RDVER4.SEQ   C G G C A T T C C T G A T C T G G A G G C C G G C G A A C T G C C T T C T G C T  1440
RDVER5.SEQ   C G G C A T T C C T G A T C T G G A G G C C G G C G A A C T G C C T T C T G C T  1440
RD7.SEQ      C G G C A T T C C T G A T C T G G A G G C C G G C G A A C T G C C T T C T G C T  1440
RDVER51.SEQ  C G G C A T T C C T G A T C T G G A G G C C G G C G A A C T G C C T T C T G C T  1440
RDVER52.SEQ  C G G C A T T C C T G A T C T G G A G G C C G G C G A A C T G C C T T C T G C T  1440
RD1561H9.SEQ C G G C A T T C C T G A T C T G G A G G C C G G C G A A C T G C C T T C T G C T  1440
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Figure 2 (cont.)

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GRVER51.SEQ  T T T G T G G T G ● A C A A C C C G G C A A G G A G A T ● C T G C T A A G G  1480
GR6.SEQ      T T T G T G G T G A A A C A A C C C G G C A A G G A G A T C A C T G C T A A G G  1480
GRVER5.SEQ   T T T G T G G T G A A A C A A C C C G G C A A G G A G A T C A C T G C T A A G G  1480
GRVER4.SEQ   T T T G T G G T G A A A C A A C C T G G A A A G G A G A T C A C T G C T A A G G  1480
GRVER3.SEQ   T T T G T G G T G A A A C A A C C T G G C A A G G A G A T T A C T G C T A A G G  1480
GRVER2.SEQ   T T T G T C G T G A A A C A A C C A G G C A A G G A A A T T A C C G C T A A A G  1480
GRVER1.SEQ   T T T G T C G T G A A A C A A C C A G G T A A G G A A A T T A C C G C T A A A G  1480
YG81-6G1.SEQ T T T G T G G T T A A A C A G C C C G G A A A G G A G A T T A C A G C T A A A G  1480
RDVER1.SEQ   T T C G T G G T C A A G C A G C C T G G C A A A G A G A T C A C T G C C A A G G  1480
RDVER2.SEQ   T T C G T G G T C A A G C A G C C T G G T A A A G A G A T C A C T G C C A A G G  1480
RDVER3.SEQ   T T C G T C G T C A A G C A G C C T G G T A A A G A A A T C A C C G C C A A A G  1480
RDVER4.SEQ   T T C G T T G T C A A G C A G C C T G G T A A A G A A A T T A C C G C C A A A G  1480
RDVER5.SEQ   T T C G T T G T C A A G C A G C C T G G T A A A G A A A T T A C C G C C A A A G  1480
RD7.SEQ      T T C G T T G T C A A G C A G C C T G G T A A A G A A A T T A C C G C C A A A G  1480
RDVER51.SEQ  T T C G T T G T C A A G C A G C C T G G T A A A G A A A T T A C C G C C A A A G  1480
RDVER52.SEQ  T T C G T T G T C A A G C A G C C T G G T A A A G A A A T T A C C G C C A A A G  1480
RD1561H9.SEQ T T C G T T G T C A A G C A G C C T G G T A C A G A A A T T A C C G C C A A A G  1480

GRVER51.SEQ  A G G T C T A C G A C T A T T T G G C C G A G C G C G T G T C T C A C A C C A A  1520
GR6.SEQ      A G G T C T A C G A C T A T T T G G C C G A G C G C G T G T C T C A C A C C A A  1520
GRVER5.SEQ   A G G T C T A C G A C T A T T T G G C C G A G C G C G T G T C T C A C A C C A A  1520
GRVER4.SEQ   A G G T C T A C G A C T A T T T G G C C G A G C G C G T G T C T C A C A C C A A  1520
GRVER3.SEQ   A G G T C T A C G A C T A T T T G G C C G A G C G C G T G T C T C A C A C T A A  1520
GRVER2.SEQ   A G G T C T A C G A C T A T T T G G C C G A G C G C G T G T C T C A C A C T A A  1520
GRVER1.SEQ   A G G T C T A C G A C T A T T T G G C C G A A C G C G T G T C T C A C A C T A A  1520
YG81-6G1.SEQ A A G T G T A C G A T T A T C T T G C C G A G A G G G T C T C C C A T A C A A  1520
RDVER1.SEQ   A A G T G T A T G A T T A C C T G G C T G A G C G T G T C A G C C A T A C C A A  1520
RDVER2.SEQ   A A G T G T A T G A T T A C C T G G C T G A A C G T G T C A G C C A T A C C A A  1520
RDVER3.SEQ   A A G T G T A T G A T T A C C T G G C T G A A C G T G T G A G C C A T A C C A A  1520
RDVER4.SEQ   A A G T G T A T G A T T A C C T G G C T G A A C G T G T G A G C C A T A C T A A  1520
RDVER5.SEQ   A A G T G T A T G A T T A C C T G G C T G A A C G T G T G A G C C A T A C T A A  1520
RD7.SEQ      A A G T G T A T G A T T A C C T G G C T G A A C G T G T G A G C C A T A C T A A  1520
RDVER51.SEQ  A A G T G T A T G A T T A C C T G G C T G A A C G T G T G A G C C A T A C T A A  1520
RDVER52.SEQ  A A G T G T A T G A T T A C C T G G C T G A A C G T G T G A G C C A T A C T A A  1520
RD1561H9.SEQ A A G T G T A T G A T T A C C T G G C T G A A C G T G T G A G C C A T A C T A A  1520

GRVER51.SEQ  A T A T C T G C G T G G C G G C G T C C G C T T C G T C G A T T C T A T T C C A  1560
GR6.SEQ      A T A T C T G C G T G G C G G C G T C C G C T T C G T C G A T T C T A T T C C A  1560
GRVER5.SEQ   A T A T C T G C G T G G C G G C G T C C G C T T C G T C G A T T C T A T T C C A  1560
GRVER4.SEQ   A T A T C T G C G T G G C G G C G T C C G C T T C G T C G A T T C C A T C C C A  1560
GRVER3.SEQ   A T A T C T G C G T G G C G G C G T C C G C T T C G T C G A T T C T A T C C C T  1560
GRVER2.SEQ   G T A C C T G C G T G G C G G T G T C C G C T T C G T C G A T A G C A T C C C T  1560
GRVER1.SEQ   G T A C C T G C G T G G C G G T G T C C G C T T C G T G G A T A G C A T C C C T  1560
YG81-6G1.SEQ G T A T T T G C G T G G A G G G G T T C G A T T C G T T G A T A G C A T A C C A  1560
RDVER1.SEQ   A T A T T T G C G C G G T G G C G T G C G T T T T G T C G A C T C T A T T C C A  1560
RDVER2.SEQ   A T A T T T G C G C G G T G G C G T G C G T T T T G T G G A C T C T A T T C C A  1560
RDVER3.SEQ   G T A C T T G C G T G G C G G C G T G C G T T T T G T G G A C A G C A T T C C A  1560
RDVER4.SEQ   G T A C T T G C G T G G C G G C G T G C G T T T T G T G G A T A G C A T T C C T  1560
RDVER5.SEQ   G T A C T T G C G T G G C G G C G T G C G T T T T G T T G A C T C C A T C C C T  1560
RD7.SEQ      G T A C T T G C G T G G C G G C G T G C G T T T T G T T G A C T C C A T C C C T  1560
RDVER51.SEQ  G T A C T T G C G T G G C G G C G T G C G T T T T G T T G A C T C C A T C C C T  1560
RDVER52.SEQ  G T A C T T G C G T G G C G G C G T G C G T T T T G T T G A C T C C A T C C C T  1560
RD1561H9.SEQ G T A C T T G C G T G G C G G C G T G C G T T T T G T T G A C T C C A T C C C T  1560
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Figure 2 (cont.)

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GRVER51.SEQ  C G C A A C G T ●  C C G G T A A G A T C A C T C G T A ●  G A G T T G C T G A  1600
GR6.SEQ      C G C A A C G T T A C C G G T A A G A T C A C T C G T A A A G A G T T G C T G A  1600
GRVER5.SEQ   C G C A A C G T T A C C G G T A A G A T C A C T C G T A A A G A G T T G C T G A  1600
GRVER4.SEQ   C G C A A C G T G A C C G G T A A G A T C A C T C G T A A A G A A T T G C T G A  1600
GRVER3.SEQ   C G C A A C G T C A C C G G C A A G A T C A C T C G T A A A G A G T T G C T G A  1600
GRVER2.SEQ   C G C A A T G T C A C C G G C A A A A T T A C T C G T A A G G A G T T G C T G A  1600
GRVER1.SEQ   C G C A A T G T C A C C G G C A A A A T T A C T C G T A A G G A G T T G C T G A  1600
YG81-6G1.SEQ A G G A A T G T T A C A G G T A A A A T T A C A A G A A A G G A A C T T C T G A  1600
RDVER1.SEQ   C G T A A C G T G A C T G G T A A G A T C A C C C G C A A A G A A C T G T T G A  1600
RDVER2.SEQ   C G T A A C G T G A C T G G T A A G A T C A C C C G C A A A G A A C T G T T G A  1600
RDVER3.SEQ   C G T A A T G T G A C T G G T A A A A T T A C C C G C A A G G A A C T G T T G A  1600
RDVER4.SEQ   C G C A A T G T G A C T G G C A A A A T T A C C C G C A A G G A G C T G T T G A  1600
RDVER5.SEQ   C G T A A C G T A A C A G G C A A A A T T A C C C G C A A G G A G C T G T T G A  1600
RD7.SEQ      C G T A A C G T A A C A G G C A A A A T T A C C C G C A A G G A G C T G T T G A  1600
RDVER51.SEQ  C G T A A C G T A A C A G G C A A A A T T A C C C G C A A G G A G C T G T T G A  1600
RDVER52.SEQ  C G T A A C G T A A C A G G C A A A A T T A C C C G C A A G G A G C T G T T G A  1600
RD1561H9.SEQ C G T A A C G T A A C A G G C A A A A T T A C C C G C A A G G A G C T G T T G A  1600
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GRVER51.SEQ  A G C A A C T C C T C G A A A A G C T G G C G G C              1626
GR6.SEQ      A G C A A C T C C T C G A A A A G C T G G C G G C              1626
GRVER5.SEQ   A G C A A C T C C T C G A A A A G C T G G C G G C              1626
GRVER4.SEQ   A G C A A C T C C T C G A A A A G C T G G C G G C              1626
GRVER3.SEQ   A A C A A T T G C T C G A A A A G C T G G C G G C              1626
GRVER2.SEQ   A A C A G T T G C T G G A A A A G G C T G G T G G C              1626
GRVER1.SEQ   A A C A G T T G C T G G A A A A G G C T G G T G G C              1626
YG81-6G1.SEQ A G C A G T T G C T G G A G A A G G C G G G A G G T              1626
RDVER1.SEQ   A G C A A C T G T T G G A G A A A G C C G G C G G T              1626
RDVER2.SEQ   A G C A A C T G T T G G A G A A A G C C G G C G G T              1626
RDVER3.SEQ   A G C A A T T G T T G G A G A A G G C C G G C G G T              1626
RDVER4.SEQ   A A C A A T T G T T G G A G A A G G C C G G C G G T              1626
RDVER5.SEQ   A A C A A T T G T T G G A G A A G G C C G G C G G T              1626
RD7.SEQ      A A C A A T T G T T G G A G A A G G C C G G C G G T              1626
RDVER51.SEQ  A A C A A T T G T T G G A G A A G G C C G G C G G T              1626
RDVER52.SEQ  A A C A A T T G T T G G A G A A G G C C G G C G G T              1626
RD1561H9.SEQ A A C A A T T G T T G G T G A A G G C C G G C G G T              1626
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Figure 3

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                 ●                                          ●
GRVER51.SEQ  M M K R E K N V I ● G P E P L H P L E D L T A G E M L ● A L R K H S H L P Q A  118
GR6.SEQ      M M K R E K N V I Y G P E P L H P L E D L T A G E M L F R A L R K H S H L P Q A  118
GRVER5.SEQ   M M K R E K N V I Y G P E P L H P L E D L T A G E M L F R A L R K H S H L P Q A  118
GRVER4.SEQ   M M K R E K N V I Y G P E P L H P L E D L T A G E M L F R A L R K H S H L P Q A  118
GRVER3.SEQ   M M K R E K N V I Y G P E P L H P L E D L T A G E M L F R A L R K H S H L P Q A  118
GRVER2.SEQ   M M K R E K N V I Y G P E P L H P L E D L T A G E M L F R A L R K H S H L P Q A  118
GRVER1.SEQ   M M K R E K N V I Y G P E P L H P L E D L T A G E M L F R A L R K H S H L P Q A  118
YG81-6G1.SEQ M M K R E K N V I Y G P E P L H P L E D L T A G E M L F R A L R K H S H L P Q A  118
RDVER1.SEQ   M M K R E K N V I Y G P E P L H P L E D L T A G E M L F R A L R K H S H L P Q A  118
RDVER2.SEQ   M M K R E K N V I Y G P E P L H P L E D L T A G E M L F R A L R K H S H L P Q A  118
RDVER3.SEQ   M M K R E K N V I Y G P E P L H P L E D L T A G E M L F R A L R K H S H L P Q A  118
RDVER4.SEQ   M M K R E K N V I Y G P E P L H P L E D L T A G E M L F R A L R K H S H L P Q A  118
RDVER5.SEQ   M M K R E K N V I Y G P E P L H P L E D L T A G E M L F R A L R K H S H L P Q A  118
RD7.SEQ      M M K R E K N V I Y G P E P L H P L E D L T A G E M L F R A L R K H S [Y] L P Q A  118
RDVER51.SEQ  M M K R E K N V I Y G P E P L H P L E D L T A G E M L F R A L R K H S H L P Q A  118
RDVER52.SEQ  M M K R E K N V I Y G P E P L H P L E D L T A G E M L F R A L R K H S H L P Q A  118
RD1561H9.SEQ M [I] K R E K N V I Y G P E P L H P L E D L T A G E M L F R A L R K H S H L P Q A  118


GRVER51.SEQ  L V D V V G D E S L S Y K E F F E A T V L L A Q S L H N C G Y K M N D V V S I C  238
GR6.SEQ      L V D V V G D E [N] L S Y K E F F E A T V L L A Q S L H N C G Y K M N D V V S I C  238
GRVER5.SEQ   L V D V V G D E S L S Y K E F F E A T V L L A Q S L H N C G Y K M N D V V S I C  238
GRVER4.SEQ   L V D V V G D E S L S Y K E F F E A T V L L A Q S L H N C G Y K M N D V V S I C  238
GRVER3.SEQ   L V D V V G D E S L S Y K E F F E A T V L L A Q S L H N C G Y K M N D V V S I C  238
GRVER2.SEQ   L V D V V G D E S L S Y K E F F E A T V L L A Q S L H N C G Y K M N D V V S I C  238
GRVER1.SEQ   L V D V V G D E S L S Y K E F F E A T V L L A Q S L H N C G Y K M N D V V S I C  238
YG81-6G1.SEQ L V D V V G D E S L S Y K E F F E A T V L L A Q S L H N C G Y K M N D V V S I C  238
RDVER1.SEQ   L V D V V G D E S L S Y K E F F E A T V L L A Q S L H N C G Y K M N D V V S I C  238
RDVER2.SEQ   L V D V V G D E S L S Y K E F F E A T V L L A Q S L H N C G Y K M N D V V S I C  238
RDVER3.SEQ   L V D V V G D E S L S Y K E F F E A T V L L A Q S L H N C G Y K M N D V V S I C  238
RDVER4.SEQ   L V D V V G D E S L S Y K E F F E A T V L L A Q S L H N C G Y K M N D V V S I C  238
RDVER5.SEQ   L V D V V G D E S L S Y K E F F E A T V L L A Q S L H N C G Y K M N D V V S I C  238
RD7.SEQ      L V D V V G D E S L S Y K E F F E A T V L L A Q S L H N C G Y K M N D V V S I C  238
RDVER51.SEQ  L V D V V G D E S L S Y K E F F E A T V L L A Q S L H N C G Y K M N D V V S I C  238
RDVER52.SEQ  L V D V V G D E S L S Y K E F F E A T V L L A Q S L H N C G Y K M N D V V S I C  238
RD1561H9.SEQ L V D V V G D E S L S Y K E F F E A T V L L A Q S L H N C G Y K M N D V V S I C  238


GRVER51.SEQ  A E N N T R F F I P V I A A W Y I G M I V A P V N E S Y I P D E L C K V M G I S  358
GR6.SEQ      A E N N T R F F I P V I A A W Y I G M I V A P V N E S Y I P D E L C K V M G I S  358
GRVER5.SEQ   A E N N T R F F I P V I A A W Y I G M I V A P V N E S Y I P D E L C K V M G I S  358
GRVER4.SEQ   A E N N T R F F I P V I A A W Y I G M I V A P V N E S Y I P D E L C K V M G I S  358
GRVER3.SEQ   A E N N T R F F I P V I A A W Y I G M I V A P V N E S Y I P D E L C K V M G I S  358
GRVER2.SEQ   A E N N T R F F I P V I A A W Y I G M I V A P V N E S Y I P D E L C K V M G I S  358
GRVER1.SEQ   A E N N T R F F I P V I A A W Y I G M I V A P V N E S Y I P D E L C K V M G I S  358
YG81-6G1.SEQ A E N N T R F F I P V I A A W Y I G M I V A P V N E S Y I P D E L C K V M G I S  358
RDVER1.SEQ   A E N N T R F F I P V I A A W Y I G M I V A P V N E S Y I P D E L C K V M G I S  358
RDVER2.SEQ   A E N N T R F F I P V I A A W Y I G M I V A P V N E S Y I P D E L C K V M G I S  358
RDVER3.SEQ   A E N N T R F F I P V I A A W Y I G M I V A P V N E S Y I P D E L C K V M G I S  358
RDVER4.SEQ   A E N N T R F F I P V I A A W Y I G M I V A P V N E S Y I P D E L C K V M G I S  358
RDVER5.SEQ   A E N N T R F F I P V I A A W Y I G M I V A P V N E S Y I P D E L C K V M G I S  358
RD7.SEQ      A E N N T R F F I P V I A A W Y I G M I V A P V N E S Y I P D E L C K V M G I S  358
RDVER51.SEQ  A E N N T R F F I P V I A A W Y I G M I V A P V N E S Y I P D E L C K V M G I S  358
RDVER52.SEQ  A E N N T R F F I P V I A A W Y I G M I V A P V N E S Y I P D E L C K V M G I S  358
RD1561H9.SEQ A E N N T R F F I P V I A A W Y I G M I V A P V N E S Y I P D E L C K V M G I S  358
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Figure 3 (cont.)

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GRVER51.SEQ   K P Q I V F T T ● I L N K V L E V Q S R T N F I K R I ● L D T V E N I H G C   478
GR6.SEQ       K P Q I V F T T K N I L N K V L E V Q S R T N F I K R I I I L D T V E N I H G C   478
GRVER5.SEQ    K P Q I V F T T K N I L N K V L E V Q S R T N F I K R I I I L D T V E N I H G C   478
GRVER4.SEQ    K P Q I V F T T K N I L N K V L E V Q S R T N F I K R I I I L D T V E N I H G C   478
GRVER3.SEQ    K P Q I V F T T K N I L N K V L E V Q S R T N F I K R I I I L D T V E N I H G C   478
GRVER2.SEQ    K P Q I V F T T K N I L N K V L E V Q S R T N F I K R I I I L D T V E N I H G C   478
GRVER1.SEQ    K P Q I V F T T K N I L N K V L E V Q S R T N F I K R I I I L D T V E N I H G C   478
YG81-6G1.SEQ  K P Q I V F T T K N I L N K V L E V Q S R T N F I K R I I I L D T V E N I H G C   478
RDVER1.SEQ    K P Q I V F T T K N I L N K V L E V Q S R T N F I K R I I I L D T V E N I H G C   478
RDVER2.SEQ    K P Q I V F T T K N I L N K V L E V Q S R T N F I K R I I I L D T V E N I H G C   478
RDVER3.SEQ    K P Q I V F T T K N I L N K V L E V Q S R T N F I K R I I I L D T V E N I H G C   478
RDVER4.SEQ    K P Q I V F T T K N I L N K V L E V Q S R T N F I K R I I I L D T V E N I H G C   478
RDVER5.SEQ    K P Q I V F T T K N I L N K V L E V Q S R T N F I K R I I I L D T V E N I H G C   478
RD7.SEQ       K P Q I V F T T K N I L N K V L E V Q S R T N F I K R I I I L D T V E N I H G C   478
RDVER51.SEQ   K P Q I V F T T K N I L N K V L E V Q S R T N F I K R I I I L D T V E N I H G C   478
RDVER52.SEQ   K P Q I V F T T K N I L N K V L E V Q S R T N F I K R I I I L D T V E N I H G C   478
RD1561H9.SEQ  K P Q I V F T T K N I L N K V L E V Q S R T N F I K R I I I L D T V E N I H G C   478

GRVER51.SEQ   E S L P N F I S R Y S D G N I A N F K P L H F D P V E Q V A A I L C S S G T T G   598
GR6.SEQ       E S L P N F I S R Y S D G N I A N F K P L H F D P V E Q V A A I L C S S G T T G   598
GRVER5.SEQ    E S L P N F I S R Y S D G N I A N F K P L H F D P V E Q V A A I L C S S G T T G   598
GRVER4.SEQ    E S L P N F I S R Y S D G N I A N F K P L H F D P V E Q V A A I L C S S G T T G   598
GRVER3.SEQ    E S L P N F I S R Y S D G N I A N F K P L H F D P V E Q V A A I L C S S G T T G   598
GRVER2.SEQ    E S L P N F I S R Y S D G N I A N F K P L H F D P V E Q V A A I L C S S G T T G   598
GRVER1.SEQ    E S L P N F I S R Y S D G N I A N F K P L H F D P V E Q V A A I L C S S G T T G   598
YG81-6G1.SEQ  E S L P N F I S R Y S D G N I A N F K P L H F D P V E Q V A A I L C S S G T T G   598
RDVER1.SEQ    E S L P N F I S R Y S D G N I A N F K P L H F D P V E Q V A A I L C S S G T T G   598
RDVER2.SEQ    E S L P N F I S R Y S D G N I A N F K P L H F D P V E Q V A A I L C S S G T T G   598
RDVER3.SEQ    E S L P N F I S R Y S D G N I A N F K P L H F D P V E Q V A A I L C S S G T T G   598
RDVER4.SEQ    E S L P N F I S R Y S D G N I A N F K P L H F D P V E Q V A A I L C S S G T T G   598
RDVER5.SEQ    E S L P N F I S R Y S D G N I A N F K P L H F D P V E Q V A A I L C S S G T T G   598
RD7.SEQ       E S L P N F I S R Y S D G N I A N F K P L H F D P V E Q V A A I L C S S G T T G   598
RDVER51.SEQ   E S L P N F I S R Y S D G N I A N F K P L H F D P V E Q V A A I L C S S G T T G   598
RDVER52.SEQ   E S L P N F I S R Y S D G N I A N F K P L H F D P V E Q V A A I L C S S G T T G   598
RD1561H9.SEQ  E S L P N F I S R Y S D G N I A N F K P L H F D P V E Q V A A I L C S S G T T G   598

GRVER51.SEQ   L P K G V M Q T H Q N I C V R L I H A L D P R [V] G T Q L I P G V T V L V Y L P F   718
GR6.SEQ       L P K G V M Q T H Q N I C V R L I H A L D P R [V] G T Q L I [S] G V T V L V Y L P F   718
GRVER5.SEQ    L P K G V M Q T H Q N I C V R L I H A L D P R [V] G T Q L I P G V T V L V Y L P F   718
GRVER4.SEQ    L P K G V M Q T H Q N I C V R L I H A L D P R [V] G T Q L I P G V T V L V Y L P F   718
GRVER3.SEQ    L P K G V M Q T H Q N I C V R L I H A L D P R [V] G T Q L I P G V T V L V Y L P F   718
GRVER2.SEQ    L P K G V M Q T H Q N I C V R L I H A L D P R [V] G T Q L I P G V T V L V Y L P F   718
GRVER1.SEQ    L P K G V M Q T H Q N I C V R L I H A L D P R [V] G T Q L I P G V T V L V Y L P F   718
YG81-6G1.SEQ  L P K G V M Q T H Q N I C V R L I H A L D P R A G T Q L I P G V T V L V Y L P F   718
RDVER1.SEQ    L P K G V M Q T H Q N I C V R L I H A L D P R [Y] G T Q L I P G V T V L V Y L P F   718
RDVER2.SEQ    L P K G V M Q T H Q N I C V R L I H A L D P R [Y] G T Q L I P G V T V L V Y L P F   718
RDVER3.SEQ    L P K G V M Q T H Q N I C V R L I H A L D P R [Y] G T Q L I P G V T V L V Y L P F   718
RDVER4.SEQ    L P K G V M Q T H Q N I C V R L I H A L D P R [Y] G T Q L I P G V T V L V Y L P F   718
RDVER5.SEQ    L P K G V M Q T H Q N I C V R L I H A L D P R [Y] G T Q L I P G V T V L V Y L P F   718
RD7.SEQ       L P K G V M Q T H Q N I C V R L I H A L D P R [Y] G T Q L I P G V T V L V Y L P F   718
RDVER51.SEQ   L P K G V M Q T H Q N I C V R L I H A L D P R [Y] G T Q L I P G V T V L V Y L P F   718
RDVER52.SEQ   L P K G V M Q T H Q N I C V R L I H A L D P R [Y] G T Q L I P G V T V L V Y L P F   718
RD1561H9.SEQ  L P K G V M Q T H Q N I C V R L I H A L D P R [Y] G T Q L I P G V T V L V Y L P F   718
```

Figure 3 (cont.)

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GRVER51.SEQ   F H A F G F S I ● G Y F M V G L R V I M F R R F D Q ●   L K A I Q D Y E V R  838
GR6.SEQ       F H A F G F S I T L G Y F M V G L R V I M F R R F D Q E A F L K A I Q D Y E V R  838
GRVER5.SEQ    F H A F G F S I T L G Y F M V G L R V I M F R R F D Q E A F L K A I Q D Y E V R  838
GRVER4.SEQ    F H A F G F S I T L G Y F M V G L R V I M F R R F D Q E A F L K A I Q D Y E V R  838
GRVER3.SEQ    F H A F G F S I T L G Y F M V G L R V I M F R R F D Q E A F L K A I Q D Y E V R  838
GRVER2.SEQ    F H A F G F S I T L G Y F M V G L R V I M F R R F D Q E A F L K A I Q D Y E V R  838
GRVER1.SEQ    F H A F G F S I T L G Y F M V G L R V I M F R R F D Q E A F L K A I Q D Y E V R  838
YG81-6G1.SEQ  F H A F G F S I T L G Y F M V G L R V I M F R R F D Q E A F L K A I Q D Y E V R  838
RDVER1.SEQ    F H A F G F |H| I T L G Y F M V G L R V I M F R R F D Q E A F L K A I Q D Y E V R  838
RDVER2.SEQ    F H A F G F |H| I T L G Y F M V G L R V I M F R R F D Q E A F L K A I Q D Y E V R  838
RDVER3.SEQ    F H A F G F |H| I T L G Y F M V G L R V I M F R R F D Q E A F L K A I Q D Y E V R  838
RDVER4.SEQ    F H A F G F |H| I T L G Y F M V G L R V I M F R R F D Q E A F L K A I Q D Y E V R  838
RDVER5.SEQ    F H A F G F |H| I T L G Y F M V G L R V I M F R R F D Q E A F L K A I Q D Y E V R  838
RD7.SEQ       F H A F G F |H| I T L G Y F M V G L R V I M F R R F D Q E A F L K A I Q D Y E V R  838
RDVER51.SEQ   F H A F G F |H| I T L G Y F M V G L R V I M F R R F D Q E A F L K A I Q D Y E V R  838
RDVER52.SEQ   F H A F G F |H| I T L G Y F M V G L R V I M F R R F D Q E A F L K A I Q D Y E V R  838
RD1561H9.SEQ  F H A F G F |H| I T L G Y F M V G L R V I M F R R F D Q E A F L K A I Q D Y E V R  838


GRVER51.SEQ   S V I N V P S V I L F L S K S P L V D K Y D L S S L R E L C C G A A P L A K E V  958
GR6.SEQ       S V I N V P S V I L F L S K S P L V D K Y D L S S L R E L C C G A A P L A K E V  958
GRVER5.SEQ    S V I N V P S V I L F L S K S P L V D K Y D L S S L R E L C C G A A P L A K E V  958
GRVER4.SEQ    S V I N V P S V I L F L S K S P L V D K Y D L S S L R E L C C G A A P L A K E V  958
GRVER3.SEQ    S V I N V P S V I L F L S K S P L V D K Y D L S S L R E L C C G A A P L A K E V  958
GRVER2.SEQ    S V I N V P S V I L F L S K S P L V D K Y D L S S L R E L C C G A A P L A K E V  958
GRVER1.SEQ    S V I N V P S V I L F L S K S P L V D K Y D L S S L R E L C C G A A P L A K E V  958
YG81-6G1.SEQ  S V I N V P S V I L F L S K S P L V D K Y D L S S L R E L C C G A A P L A K E V  958
RDVER1.SEQ    S V I N V P S V I L F L S K S P L V D K Y D L S S L R E L C C G A A P L A K E V  958
RDVER2.SEQ    S V I N V P S V I L F L S K S P L V D K Y D L S S L R E L C C G A A P L A K E V  958
RDVER3.SEQ    S V I N V P S V I L F L S K S P L V D K Y D L S S L R E L C C G A A P L A K E V  958
RDVER4.SEQ    S V I N V P S V I L F L S K S P L V D K Y D L S S L R E L C C G A A P L A K E V  958
RDVER5.SEQ    S V I N V P S V I L F L S K S P L V D K Y D L S S L R E L C C G A A P L A K E V  958
RD7.SEQ       S V I N V P S V I L F L S K S P L V D K Y D L S S L R E L C C G A A P L A K E V  958
RDVER51.SEQ   S V I N V P S V I L F L S K S P L V D K Y D L S S L R E L C C G A A P L A K E V  958
RDVER52.SEQ   S V I N V P S V I L F L S K S P L V D K Y D L S S L R E L C C G A A P L A K E V  958
RD1561H9.SEQ  S V I N V P S V I L F L S K S P L V D K Y D L S S L R E L C C G A A P L A K E V  958


GRVER51.SEQ   A E V A A K R L N L P G I R C G F G L T E S T S A N I H S L R D E F K S G S L G  1078
GR6.SEQ       A E V A A K R L N L P G I R C G F G L T E S T S A N I H S L R D E F K S G S L G  1078
GRVER5.SEQ    A E V A A K R L N L P G I R C G F G L T E S T S A N I H S L R D E F K S G S L G  1078
GRVER4.SEQ    A E V A A K R L N L P G I R C G F G L T E S T S A N I H S L R D E F K S G S L G  1078
GRVER3.SEQ    A E V A A K R L N L P G I R C G F G L T E S T S A N I H S L R D E F K S G S L G  1078
GRVER2.SEQ    A E V A A K R L N L P G I R C G F G L T E S T S A N I H S L R D E F K S G S L G  1078
GRVER1.SEQ    A E V A A K R L N L P G I R C G F G L T E S T S A N I H S L R D E F K S G S L G  1078
YG81-6G1.SEQ  A E V A A K R L N L P G I R C G F G L T E S T S A N I H S L R D E F K S G S L G  1078
RDVER1.SEQ    A E V A A K R L N L P G I R C G F G L T E S T S A |I| I |Q| S L R D E F K S G S L G  1078
RDVER2.SEQ    A E V A A K R L N L P G I R C G F G L T E S T S A |I| I |Q| S L R D E F K S G S L G  1078
RDVER3.SEQ    A E V A A K R L N L P G I R C G F G L T E S T S A |I| I |Q| S L R D E F K S G S L G  1078
RDVER4.SEQ    A E V A A K R L N L P G I R C G F G L T E S T S A |I| I |Q| S L R D E F K S G S L G  1078
RDVER5.SEQ    A E V A A K R L N L P G I R C G F G L T E S T S A |I| I |Q| S L R D E F K S G S L G  1078
RD7.SEQ       A E V A A K R L N L P G I R C G F G L T E S T S A |I| I |Q| S L R D E F K S G S L G  1078
RDVER51.SEQ   A E V A A K R L N L P G I R C G F G L T E S T S A |I| I |Q| S L R D E F K S G S L G  1078
RDVER52.SEQ   A E V A A K R L N L P G I R C G F G L T E S T S A |I| I |Q| S L |G| D E F K S G S L G  1078
RD1561H9.SEQ  A E V A A K R L N L P G I R C G F G L T E S T S A |I| I |Q T| L |G| D E F K S G S L G  1078
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Figure 3 (cont.)

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GRVER51.SEQ   R V T P L M A A ● A D R E T G K A L G P N Q V G E L ● K G P M V S K G Y V N   1198
GR6.SEQ       R V T P L M A A K I A D R E T G K A L G P N Q V G E L C I K G P M V S K G Y V N   1198
GRVER5.SEQ    R V T P L M A A K I A D R E T G K A L G P N Q V G E L C I K G P M V S K G Y V N   1198
GRVER4.SEQ    R V T P L M A A K I A D R E T G K A L G P N Q V G E L C I K G P M V S K G Y V N   1198
GRVER3.SEQ    R V T P L M A A K I A D R E T G K A L G P N Q V G E L C I K G P M V S K G Y V N   1198
GRVER2.SEQ    R V T P L M A A K I A D R E T G K A L G P N Q V G E L C I K G P M V S K G Y V N   1198
GRVER1.SEQ    R V T P L M A A K I A D R E T G K A L G P N Q V G E L C I K G P M V S K G Y V N   1198
YG81-6G1.SEQ  R V T P L M A A K I A D R E T G K A L G P N Q V G E L C I K G P M V S K G Y V N   1198
RDVER1.SEQ    R V T P L M A A K I A D R E T G K A L G P N Q V G E L C I K G P M V S K G Y V N   1198
RDVER2.SEQ    R V T P L M A A K I A D R E T G K A L G P N Q V G E L C I K G P M V S K G Y V N   1198
RDVER3.SEQ    R V T P L M A A K I A D R E T G K A L G P N Q V G E L C I K G P M V S K G Y V N   1198
RDVER4.SEQ    R V T P L M A A K I A D R E T G K A L G P N Q V G E L C I K G P M V S K G Y V N   1198
RDVER5.SEQ    R V T P L M A A K I A D R E T G K A L G P N Q V G E L C I K G P M V S K G Y V N   1198
RD7.SEQ       R V T P L M A A K I A D R E T G K A L G P N Q V G E L C I K G P M V S K G Y V N   1198
RDVER51.SEQ   R V T P L M A A K I A D R E T G K A L G P N Q V G E L C I K G P M V S K G Y V N   1198
RDVER52.SEQ   R V T P L M A A K I A D R E T G K A L G P N Q V G E L C I K G P M V S K G Y V N   1198
RD1561H9.SEQ  R V T P L M A A K I A D R E T G K A L G P N Q V G E L C I K G P M V S K G Y V N   1198


GRVER51.SEQ   N V E A T K E A I D D D G W L H S G D F G Y Y D E D E H F Y V V D R Y K E L I K   1318
GR6.SEQ       N V E A T K E A I D D D G W L H S G D F G Y Y D E D E H F Y V V D R Y K E L I K   1318
GRVER5.SEQ    N V E A T K E A I D D D G W L H S G D F G Y Y D E D E H F Y V V D R Y K E L I K   1318
GRVER4.SEQ    N V E A T K E A I D D D G W L H S G D F G Y Y D E D E H F Y V V D R Y K E L I K   1318
GRVER3.SEQ    N V E A T K E A I D D D G W L H S G D F G Y Y D E D E H F Y V V D R Y K E L I K   1318
GRVER2.SEQ    N V E A T K E A I D D D G W L H S G D F G Y Y D E D E H F Y V V D R Y K E L I K   1318
GRVER1.SEQ    N V E A T K E A I D D D G W L H S G D F G Y Y D E D E H F Y V V D R Y K E L I K   1318
YG81-6G1.SEQ  N V E A T K E A I D D D G W L H S G D F G Y Y D E D E H F Y V V D R Y K E L I K   1318
RDVER1.SEQ    N V E A T K E A I D D D G W L H S G D F G Y Y D E D E H F Y V V D R Y K E L I K   1318
RDVER2.SEQ    N V E A T K E A I D D D G W L H S G D F G Y Y D E D E H F Y V V D R Y K E L I K   1318
RDVER3.SEQ    N V E A T K E A I D D D G W L H S G D F G Y Y D E D E H F Y V V D R Y K E L I K   1318
RDVER4.SEQ    N V E A T K E A I D D D G W L H S G D F G Y Y D E D E H F Y V V D R Y K E L I K   1318
RDVER5.SEQ    N V E A T K E A I D D D G W L H S G D F G Y Y D E D E H F Y V V D R Y K E L I K   1318
RD7.SEQ       N V E A T K E A I D D D G W L H S G D F G Y Y D E D E H F Y V V D R Y K E L I K   1318
RDVER51.SEQ   N V E A T K E A I D D D G W L H S G D F G Y Y D E D E H F Y V V D R Y K E L I K   1318
RDVER52.SEQ   N V E A T K E A I D D D G W L H S G D F G Y Y D E D E H F Y V V D R Y K E L I K   1318
RD1561H9.SEQ  N V E A T K E A I D D D G W L H S G D F G Y Y D E D E H F Y V V D R Y K E L I K   1318


GRVER51.SEQ   Y K G S Q V A P A E L E E I L L K N P C I R D V A V V G I P D L E A G E L P S A   1438
GR6.SEQ       Y K G S Q V A P A E L E E I L L K N P C I R D V A V V G I P D L E A G E L P S A   1438
GRVER5.SEQ    Y K G S Q V A P A E L E E I L L K N P C I R D V A V V G I P D L E A G E L P S A   1438
GRVER4.SEQ    Y K G S Q V A P A E L E E I L L K N P C I R D V A V V G I P D L E A G E L P S A   1438
GRVER3.SEQ    Y K G S Q V A P A E L E E I L L K N P C I R D V A V V G I P D L E A G E L P S A   1438
GRVER2.SEQ    Y K G S Q V A P A E L E E I L L K N P C I R D V A V V G I P D L E A G E L P S A   1438
GRVER1.SEQ    Y K G S Q V A P A E L E E I L L K N P C I R D V A V V G I P D L E A G E L P S A   1438
YG81-6G1.SEQ  Y K G S Q V A P A E L E E I L L K N P C I R D V A V V G I P D L E A G E L P S A   1438
RDVER1.SEQ    Y K G S Q V A P A E L E E I L L K N P C I R D V A V V G I P D L E A G E L P S A   1438
RDVER2.SEQ    Y K G S Q V A P A E L E E I L L K N P C I R D V A V V G I P D L E A G E L P S A   1438
RDVER3.SEQ    Y K G S Q V A P A E L E E I L L K N P C I R D V A V V G I P D L E A G E L P S A   1438
RDVER4.SEQ    Y K G S Q V A P A E L E E I L L K N P C I R D V A V V G I P D L E A G E L P S A   1438
RDVER5.SEQ    Y K G S Q V A P A E L E E I L L K N P C I R D V A V V G I P D L E A G E L P S A   1438
RD7.SEQ       Y K G S Q V A P A E L E E I L L K N P C I R D V A V V G I P D L E A G E L P S A   1438
RDVER51.SEQ   Y K G S Q V A P A E L E E I L L K N P C I R D V A V V G I P D L E A G E L P S A   1438
RDVER52.SEQ   Y K G S Q V A P A E L E E I L L K N P C I R D V A V V G I P D L E A G E L P S A   1438
RD1561H9.SEQ  Y K G S Q V A P A E L E E I L L K N P C I R D V A V V G I P D L E A G E L P S A   1438
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Figure 3 (cont.)

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GRVER51.SEQ  F V V K Q P G K E ● A K E V Y D Y L A E R V S H T K Y ● G G V R F V D S I P  1558
GR6.SEQ      F V V K Q P G K E I T A K E V Y D Y L A E R V S H T K Y L R G G V R F V D S I P  1558
GRVER5.SEQ   F V V K Q P G K E I T A K E V Y D Y L A E R V S H T K Y L R G G V R F V D S I P  1558
GRVER4.SEQ   F V V K Q P G K E I T A K E V Y D Y L A E R V S H T K Y L R G G V R F V D S I P  1558
GRVER3.SEQ   F V V K Q P G K E I T A K E V Y D Y L A E R V S H T K Y L R G G V R F V D S I P  1558
GRVER2.SEQ   F V V K Q P G K E I T A K E V Y D Y L A E R V S H T K Y L R G G V R F V D S I P  1558
GRVER1.SEQ   F V V K Q P G K E I T A K E V Y D Y L A E R V S H T K Y L R G G V R F V D S I P  1558
YG81-6G1.SEQ F V V K Q P G K E I T A K E V Y D Y L A E R V S H T K Y L R G G V R F V D S I P  1558
RDVER1.SEQ   F V V K Q P G K E I T A K E V Y D Y L A E R V S H T K Y L R G G V R F V D S I P  1558
RDVER2.SEQ   F V V K Q P G K E I T A K E V Y D Y L A E R V S H T K Y L R G G V R F V D S I P  1558
RDVER3.SEQ   F V V K Q P G K E I T A K E V Y D Y L A E R V S H T K Y L R G G V R F V D S I P  1558
RDVER4.SEQ   F V V K Q P G K E I T A K E V Y D. Y L A E R V S H T K Y L R G G V R F V D S I P  1558
RDVER5.SEQ   F V V K Q P G K E I T A K E V Y D Y L A E R V S H T K Y L R G G V R F V D S I P  1558
RD7.SEQ      F V V K Q P G K E I T A K E V Y D Y L A E R V S H T K Y L R G G V R F V D S I P  1558
RDVER51.SEQ  F V V K Q P G K E I T A K E V Y D Y L A E R V S H T K Y L R G G V R F V D S I P  1558
RDVER52.SEQ  F V V K Q P G K E I T A K E V Y D Y L A E R V S H T K Y L R G G V R F V D S I P  1558
RD1561H9.SEQ F V V K Q P G [T] E I T A K E V Y D Y L A E R V S H T K Y L R G G V R F V D S I P  1558

GRVER51.SEQ  R N V T G K I T R K E L L K Q L L E K A G G                                    1624
GR6.SEQ      R N V T G K I T R K E L L K Q L L E K A G G                                    1624
GRVER5.SEQ   R N V T G K I T R K E L L K Q L L E K A G G                                    1624
GRVER4.SEQ   R N V T G K I T R K E L L K Q L L E K A G G                                    1624
GRVER3.SEQ   R N V T G K I T R K E L L K Q L L E K A G G                                    1624
GRVER2.SEQ   R N V T G K I T R K E L L K Q L L E K A G G                                    1624
GRVER1.SEQ   R N V T G K I T R K E L L K Q L L E K A G G                                    1624
YG81-6G1.SEQ R N V T G K I T R K E L L K Q L L E K A G G                                    1624
RDVER1.SEQ   R N V T G K I T R K E L L K Q L L E K A G G                                    1624
RDVER2.SEQ   R N V T G K I T R K E L L K Q L L E K A G G                                    1624
RDVER3.SEQ   R N V T G K I T R K E L L K Q L L E K A G G                                    1624
RDVER4.SEQ   R N V T G K I T R K E L L K Q L L E K A G G                                    1624
RDVER5.SEQ   R N V T G K I T R K E L L K Q L L E K A G G                                    1624
RD7.SEQ      R N V T G K I T R K E L L K Q L L E K A G G                                    1624
RDVER51.SEQ  R N V T G K I T R K E L L K Q L L E K A G G                                    1624
RDVER52.SEQ  R N V T G K I T R K E L L K Q L L E K A G G                                    1624
RD1561H9.SEQ R N V T G K I T R K E L L K Q L L [V] K A G G                                    1624
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Figure 4 Codon Usage Analysis

per 542 total codons

	YG#81-6G	ver1 GR	ver1 RD	ver5 GR	ver5 RD	HUM
CGA	7	0	0	2	0	3
CGC	1	13	13	11	12	6
CGG	0	0	0	0	0	6
CGT	5	13	13	13	14	3
AGA	6	0	0	0	0	5
Arg AGG	7	0	0	0	0	6
CTA	5	0	0	0	0	3
CTC	4	0	1	12	11	11
CTG	4	28	27	19	18	23
CTT	12	0	0	1	1	6
TTA	17	0	0	0	0	3
Leu TTG	13	27	27	23	25	6
TCA	6	0	0	1	2	5
TCC	2	0	0	4	2	10
TCG	7	0	0	0	0	2
TCT	7	16	15	11	12	7
AGC	2	15	15	14	12	10
Ser AGT	7	0	0	1	2	5
ACA	10	0	0	0	1	8
ACC	2	11	11	8	11	12
ACG	2	0	0	0	0	4
Thr ACT	8	11	11	14	10	7
CCA	9	14	14	9	12	8
CCC	8	0	0	2	1	11
CCG	2	0	0	0	0	4
Pro CCT	9	14	14	17	15	8
GCA	14	0	0	5	4	8
GCC	4	19	18	14	12	16
GCG	5	0	0	0	0	4
Ala GCT	15	18	19	18	21	11
GGA	18	0	0	1	3	9
GGC	3	20	19	21	21	14
GGG	2	0	0	1	1	9
Gly GGT	16	19	20	16	14	6
GTA	13	0	0	1	1	3
GTC	4	25	24	21	26	9
GTG	12	25	25	25	17	17
Val GTT	20	0	0	3	5	6
AAA	23	17	18	19	13	12
Lys AAG	12	18	17	16	22	19
AAC	6	11	11	13	12	12
Asn AAT	16	11	10	9	9	9
CAA	8	7	8	11	7	6
Gln CAG	6	7	7	3	8	18
CAC	6	7	6	7	4	8
His CAT	7	6	7	6	9	5
GAA	26	19	19	19	18	15
Glu GAG	12	19	19	19	20	22
GAC	6	13	13	14	12	16
Asp GAT	20	13	13	12	14	12
TAC	8	10	10	12	13	10
Tyr TAT	11	9	10	7	7	7
TGC	3	6	5	3	4	8
Cys TGT	8	5	6	8	7	5
TTC	11	13	12	15	12	12
Phe TTT	14	12	13	10	13	9
ATA	12	0	0	0	0	3
ATC	7	19	19	23	20	13
Ile ATT	19	19	20	15	19	8
Met ATG	11	11	11	11	11	12
Trp TGG	2	2	2	2	2	7

relative codon usage for each aa (*100)

	YG#81-6G	ver5 GR	ver5 RD	HUM
CGA	27	8	0	10
CGC	4	42	46	21
CGG	0	0	0	19
CGT	19	50	54	9
AGA	23	0	0	19
Arg AGG	27	0	0	21
CTA	9	0	0	6
CTC	7	22	20	21
CTG	7	35	33	44
CTT	22	2	2	11
TTA	31	0	0	6
Leu TTG	24	42	45	11
TCA	19	3	7	13
TCC	6	13	7	25
TCG	23	0	0	6
TCT	23	35	40	18
AGC	6	45	40	26
Ser AGT	23	3	7	13
ACA	45	0	5	25
ACC	9	36	50	40
ACG	9	0	0	12
Thr ACT	36	64	45	22
CCA	32	32	43	26
CCC	29	7	4	35
CCG	7	0	0	12
Pro CCT	32	61	54	27
GCA	37	13	11	19
GCC	11	37	32	40
GCG	13	0	0	10
Ala GCT	39	47	55	27
GGA	46	3	8	24
GGC	8	54	54	36
GGG	5	3	3	25
Gly GGT	41	41	36	16
GTA	27	2	2	9
GTC	8	42	53	25
GTG	24	50	35	48
Val GTT	41	6	10	16
AAA	66	54	37	39
Lys AAG	34	46	63	61
AAC	27	59	57	58
Asn AAT	73	41	43	43
CAA	57	79	47	25
Gln CAG	43	21	53	76
CAC	46	54	31	59
His CAT	54	46	69	39
GAA	68	50	47	39
Glu GAG	32	50	53	61
GAC	23	54	46	56
Asp GAT	77	46	54	42
TAC	42	63	65	60
Tyr TAT	58	37	35	40
TGC	27	27	36	60
Cys TGT	73	73	64	41
TTC	44	60	48	58
Phe TTT	56	40	52	41
ATA	32	0	0	13
ATC	18	61	51	55
Ile ATT	50	39	49	34
Met ATG	100	100	100	100
Trp TGG	100	100	100	100

Figure 5A

Codon Usage YG#81-6G01 (yellow-green)

TTT	Phe	14	TCT	Ser	7	TAT	Tyr	11	TGT	Cys	8
TTC	Phe	11	TCC	Ser	2	TAC	Tyr	8	TGC	Cys	3
TTA	Leu	17	TCA	Ser	6	TAA	***	0	TGA	***	0
TTG	Leu	13	TCG	Ser	7	TAG	***	0	TGG	Trp	2
CTT	Leu	12	CCT	Pro	9	CAT	His	7	CGT	Arg	5
CTC	Leu	4	CCC	Pro	8	CAC	His	6	CGC	Arg	1
CTA	Leu	5	CCA	Pro	9	CAA	Gln	8	CGA	Arg	7
CTG	Leu	4	CCG	Pro	2	CAG	Gln	6	CGG	Arg	0
ATT	Ile	19	ACT	Thr	8	AAT	Asn	16	AGT	Ser	7
ATC	Ile	7	ACC	Thr	2	AAC	Asn	6	AGC	Ser	2
ATA	Ile	12	ACA	Thr	10	AAA	Lys	23	AGA	Arg	6
ATG	Met	11	ACG	Thr	2	AAG	Lys	12	AGG	Arg	7
GTT	Val	20	GCT	Ala	15	GAT	Asp	20	GGT	Gly	16
GTC	Val	4	GCC	Ala	4	GAC	Asp	6	GGC	Gly	3
GTA	Val	13	GCA	Ala	14	GAA	Glu	26	GGA	Gly	18
GTG	Val	12	GCG	Ala	5	GAG	Glu	12	GGG	Gly	2

Figure 5B

Codon Usage: GRver1

TTT	Phe	12	TCT	Ser	16	TAT	Tyr	9	TGT	Cys	5
TTC	Phe	13	TCC	Ser	0	TAC	Tyr	10	TGC	Cys	6
TTA	Leu	0	TCA	Ser	0	TAA	***	0	TGA	***	0
TTG	Leu	27	TCG	Ser	0	TAG	***	0	TGG	Trp	2
CTT	Leu	0	CCT	Pro	14	CAT	His	6	CGT	Arg	13
CTC	Leu	0	CCC	Pro	0	CAC	His	7	CGC	Arg	13
CTA	Leu	0	CCA	Pro	14	CAA	Gln	7	CGA	Arg	0
CTG	Leu	28	CCG	Pro	0	CAG	Gln	7	CGG	Arg	0
ATT	Ile	19	ACT	Thr	11	AAT	Asn	11	AGT	Ser	0
ATC	Ile	19	ACC	Thr	11	AAC	Asn	11	AGC	Ser	15
ATA	Ile	0	ACA	Thr	0	AAA	Lys	17	AGA	Arg	0
ATG	Met	11	ACG	Thr	0	AAG	Lys	18	AGG	Arg	0
GTT	Val	0	GCT	Ala	18	GAT	Asp	13	GGT	Gly	19
GTC	Val	25	GCC	Ala	19	GAC	Asp	13	GGC	Gly	20
GTA	Val	0	GCA	Ala	0	GAA	Glu	19	GGA	Gly	0
GTG	Val	25	GCG	Ala	0	GAG	Glu	19	GGG	Gly	0

Figure 5C

Codon Usage: RDver1

TTT	Phe	13	TCT	Ser	15	TAT	Tyr	10	TGT	Cys	6
TTC	Phe	12	TCC	Ser	0	TAC	Tyr	10	TGC	Cys	5
TTA	Leu	0	TCA	Ser	0	TAA	***	0	TGA	***	0
TTG	Leu	27	TCG	Ser	0	TAG	***	0	TGG	Trp	2
CTT	Leu	0	CCT	Pro	14	CAT	His	7	CGT	Arg	13
CTC	Leu	1	CCC	Pro	0	CAC	His	6	CGC	Arg	13
CTA	Leu	0	CCA	Pro	14	CAA	Gln	8	CGA	Arg	0
CTG	Leu	27	CCG	Pro	0	CAG	Gln	7	CGG	Arg	0
ATT	Ile	20	ACT	Thr	11	AAT	Asn	10	AGT	Ser	0
ATC	Ile	19	ACC	Thr	11	AAC	Asn	11	AGC	Ser	15
ATA	Ile	0	ACA	Thr	0	AAA	Lys	18	AGA	Arg	0
ATG	Met	11	ACG	Thr	0	AAG	Lys	17	AGG	Arg	0
GTT	Val	0	GCT	Ala	19	GAT	Asp	13	GGT	Gly	20
GTC	Val	24	GCC	Ala	18	GAC	Asp	13	GGC	Gly	19
GTA	Val	0	GCA	Ala	0	GAA	Glu	19	GGA	Gly	0
GTG	Val	25	GCG	Ala	0	GAG	Glu	19	GGG	Gly	0

Figure 5D

Codon Usage: Grver2

TTT	Phe	12	TCT	Ser	15	TAT	Tyr	9	TGT	Cys	5
TTC	Phe	13	TCC	Ser	0	TAC	Tyr	10	TGC	Cys	6
TTA	Leu	0	TCA	Ser	0	TAA	***	0	TGA	***	0
TTG	Leu	27	TCG	Ser	0	TAG	***	0	TGG	Trp	2
CTT	Leu	0	CCT	Pro	14	CAT	His	6	CGT	Arg	13
CTC	Leu	0	CCC	Pro	0	CAC	His	7	CGC	Arg	13
CTA	Leu	0	CCA	Pro	14	CAA	Gln	10	CGA	Arg	0
CTG	Leu	28	CCG	Pro	0	CAG	Gln	4	CGG	Arg	0
ATT	Ile	20	ACT	Thr	11	AAT	Asn	11	AGT	Ser	0
ATC	Ile	18	ACC	Thr	11	AAC	Asn	11	AGC	Ser	16
ATA	Ile	0	ACA	Thr	0	AAA	Lys	16	AGA	Arg	0
ATG	Met	11	ACG	Thr	0	AAG	Lys	19	AGG	Arg	0
GTT	Val	0	GCT	Ala	18	GAT	Asp	13	GGT	Gly	18
GTC	Val	28	GCC	Ala	19	GAC	Asp	13	GGC	Gly	21
GTA	Val	0	GCA	Ala	0	GAA	Glu	17	GGA	Gly	0
GTG	Val	22	GCG	Ala	0	GAG	Glu	21	GGG	Gly	0

Figure 5E

Codon Usage:Rdver2

TTT	Phe	13	TCT	Ser	16	TAT	Tyr	10	TGT	Cys	6
TTC	Phe	12	TCC	Ser	0	TAC	Tyr	10	TGC	Cys	5
TTA	Leu	0	TCA	Ser	0	TAA	***	0	TGA	***	0
TTG	Leu	27	TCG	Ser	0	TAG	***	0	TGG	Trp	2
CTT	Leu	0	CCT	Pro	15	CAT	His	7	CGT	Arg	13
CTC	Leu	1	CCC	Pro	0	CAC	His	6	CGC	Arg	13
CTA	Leu	0	CCA	Pro	13	CAA	Gln	8	CGA	Arg	0
CTG	Leu	27	CCG	Pro	0	CAG	Gln	7	CGG	Arg	0
ATT	Ile	19	ACT	Thr	11	AAT	Asn	10	AGT	Ser	0
ATC	Ile	20	ACC	Thr	11	AAC	Asn	11	AGC	Ser	14
ATA	Ile	0	ACA	Thr	0	AAA	Lys	19	AGA	Arg	0
ATG	Met	11	ACG	Thr	0	AAG	Lys	16	AGG	Arg	0
GTT	Val	0	GCT	Ala	19	GAT	Asp	13	GGT	Gly	21
GTC	Val	21	GCC	Ala	17	GAC	Asp	13	GGC	Gly	18
GTA	Val	0	GCA	Ala	1	GAA	Glu	21	GGA	Gly	0
GTG	Val	28	GCG	Ala	0	GAG	Glu	17	GGG	Gly	0

Figure 5F

Codon Usage: GRver3

TTT	Phe	13	TCT	Ser	16	TAT	Tyr	9	TGT	Cys	7
TTC	Phe	12	TCC	Ser	0	TAC	Tyr	10	TGC	Cys	4
TTA	Leu	0	TCA	Ser	0	TAA	***	0	TGA	***	0
TTG	Leu	26	TCG	Ser	0	TAG	***	0	TGG	Trp	2
CTT	Leu	0	CCT	Pro	18	CAT	His	6	CGT	Arg	14
CTC	Leu	5	CCC	Pro	0	CAC	His	7	CGC	Arg	12
CTA	Leu	0	CCA	Pro	10	CAA	Gln	9	CGA	Arg	0
CTG	Leu	24	CCG	Pro	0	CAG	Gln	5	CGG	Arg	0
ATT	Ile	14	ACT	Thr	14	AAT	Asn	11	AGT	Ser	0
ATC	Ile	24	ACC	Thr	8	AAC	Asn	11	AGC	Ser	15
ATA	Ile	0	ACA	Thr	0	AAA	Lys	21	AGA	Arg	0
ATG	Met	11	ACG	Thr	0	AAG	Lys	14	AGG	Arg	0
GTT	Val	1	GCT	Ala	18	GAT	Asp	12	GGT	Gly	18
GTC	Val	22	GCC	Ala	18	GAC	Asp	14	GGC	Gly	21
GTA	Val	0	GCA	Ala	1	GAA	Glu	20	GGA	Gly	0
GTG	Val	27	GCG	Ala	0	GAG	Glu	18	GGG	Gly	0

Figure 5G

Codon Usage: RDver3

TTT	Phe	13	TCT	Ser	14	TAT	Tyr	7	TGT	Cys	6	
TTC	Phe	12	TCC	Ser	1	TAC	Tyr	13	TGC	Cys	5	
TTA	Leu	0	TCA	Ser	0	TAA	***	0	TGA	***	0	
TTG	Leu	27	TCG	Ser	0	TAG	***	0	TGG	Trp	2	
CTT	Leu	0	CCT	Pro	16	CAT	His	10	CGT	Arg	16	
CTC	Leu	6	CCC	Pro	0	CAC	His	3	CGC	Arg	10	
CTA	Leu	0	CCA	Pro	12	CAA	Gln	8	CGA	Arg	0	
CTG	Leu	22	CCG	Pro	0	CAG	Gln	7	CGG	Arg	0	
ATT	Ile	20	ACT	Thr	10	AAT	Asn	10	AGT	Ser	0	
ATC	Ile	19	ACC	Thr	12	AAC	Asn	11	AGC	Ser	15	
ATA	Ile	0	ACA	Thr	0	AAA	Lys	13	AGA	Arg	0	
ATG	Met	11	ACG	Thr	0	AAG	Lys	22	AGG	Arg	0	
GTT	Val	0	GCT	Ala	20	GAT	Asp	14	GGT	Gly	16	
GTC	Val	27	GCC	Ala	16	GAC	Asp	12	GGC	Gly	23	
GTA	Val	0	GCA	Ala	1	GAA	Glu	18	GGA	Gly	0	
GTG	Val	22	GCG	Ala	0	GAG	Glu	20	GGG	Gly	0	

Figure 5H

Codon Usage: GRver4

TTT	Phe	11	TCT	Ser	13	TAT	Tyr	7	TGT	Cys	8
TTC	Phe	14	TCC	Ser	2	TAC	Tyr	12	TGC	Cys	3
TTA	Leu	0	TCA	Ser	1	TAA	***	0	TGA	***	0
TTG	Leu	21	TCG	Ser	0	TAG	***	0	TGG	Trp	2
CTT	Leu	1	CCT	Pro	18	CAT	His	7	CGT	Arg	14
CTC	Leu	11	CCC	Pro	0	CAC	His	6	CGC	Arg	11
CTA	Leu	0	CCA	Pro	10	CAA	Gln	11	CGA	Arg	1
CTG	Leu	22	CCG	Pro	0	CAG	Gln	3	CGG	Arg	0
ATT	Ile	13	ACT	Thr	14	AAT	Asn	11	AGT	Ser	1
ATC	Ile	25	ACC	Thr	8	AAC	Asn	11	AGC	Ser	14
ATA	Ile	0	ACA	Thr	0	AAA	Lys	20	AGA	Arg	0
ATG	Met	11	ACG	Thr	0	AAG	Lys	15	AGG	Arg	0
GTT	Val	3	GCT	Ala	19	GAT	Asp	12	GGT	Gly	17
GTC	Val	22	GCC	Ala	15	GAC	Asp	14	GGC	Gly	19
GTA	Val	0	GCA	Ala	3	GAA	Glu	20	GGA	Gly	3
GTG	Val	25	GCG	Ala	0	GAG	Glu	18	GGG	Gly	0

Figure 5I

Codon Usage: RDver4

TTT	Phe	13	TCT	Ser	11	TAT	Tyr	7	TGT	Cys	7
TTC	Phe	12	TCC	Ser	2	TAC	Tyr	13	TGC	Cys	4
TTA	Leu	0	TCA	Ser	2	TAA	***	0	TGA	***	0
TTG	Leu	28	TCG	Ser	0	TAG	***	0	TGG	Trp	2
CTT	Leu	0	CCT	Pro	16	CAT	His	11	CGT	Arg	15
CTC	Leu	7	CCC	Pro	2	CAC	His	2	CGC	Arg	11
CTA	Leu	0	CCA	Pro	10	CAA	Gln	7	CGA	Arg	0
CTG	Leu	20	CCG	Pro	0	CAG	Gln	8	CGG	Arg	0
ATT	Ile	21	ACT	Thr	11	AAT	Asn	10	AGT	Ser	1
ATC	Ile	18	ACC	Thr	11	AAC	Asn	11	AGC	Ser	14
ATA	Ile	0	ACA	Thr	0	AAA	Lys	13	AGA	Arg	0
ATG	Met	11	ACG	Thr	0	AAG	Lys	22	AGG	Arg	0
GTT	Val	3	GCT	Ala	22	GAT	Asp	15	GGT	Gly	14
GTC	Val	27	GCC	Ala	11	GAC	Asp	11	GGC	Gly	21
GTA	Val	0	GCA	Ala	4	GAA	Glu	18	GGA	Gly	4
GTG	Val	19	GCG	Ala	0	GAG	Glu	20	GGG	Gly	0

Figure 5J

Codon Usage: GRver5

TTT	Phe	10	TCT	Ser	11	TAT	Tyr	7	TGT	Cys	8
TTC	Phe	15	TCC	Ser	4	TAC	Tyr	12	TGC	Cys	3
TTA	Leu	0	TCA	Ser	1	TAA	***	0	TGA	***	0
TTG	Leu	23	TCG	Ser	0	TAG	***	0	TGG	Trp	2
CTT	Leu	1	CCT	Pro	17	CAT	His	6	CGT	Arg	13
CTC	Leu	12	CCC	Pro	2	CAC	His	7	CGC	Arg	11
CTA	Leu	0	CCA	Pro	9	CAA	Gln	11	CGA	Arg	2
CTG	Leu	19	CCG	Pro	0	CAG	Gln	3	CGG	Arg	0
ATT	Ile	15	ACT	Thr	14	AAT	Asn	9	AGT	Ser	1
ATC	Ile	23	ACC	Thr	8	AAC	Asn	13	AGC	Ser	14
ATA	Ile	0	ACA	Thr	0	AAA	Lys	19	AGA	Arg	0
ATG	Met	11	ACG	Thr	0	AAG	Lys	16	AGG	Arg	0
GTT	Val	3	GCT	Ala	18	GAT	Asp	12	GGT	Gly	16
GTC	Val	21	GCC	Ala	14	GAC	Asp	14	GGC	Gly	21
GTA	Val	1	GCA	Ala	5	GAA	Glu	19	GGA	Gly	1
GTG	Val	25	GCG	Ala	0	GAG	Glu	19	GGG	Gly	1

Figure 5K

Codon Usage: RDver5

TTT	Phe	13	TCT	Ser	12	TAT	Tyr	7	TGT	Cys	7
TTC	Phe	12	TCC	Ser	2	TAC	Tyr	13	TGC	Cys	4
TTA	Leu	0	TCA	Ser	2	TAA	***	0	TGA	***	0
TTG	Leu	25	TCG	Ser	0	TAG	***	0	TGG	Trp	2
CTT	Leu	1	CCT	Pro	15	CAT	His	9	CGT	Arg	14
CTC	Leu	11	CCC	Pro	1	CAC	His	4	CGC	Arg	12
CTA	Leu	0	CCA	Pro	12	CAA	Gln	7	CGA	Arg	0
CTG	Leu	18	CCG	Pro	0	CAG	Gln	8	CGG	Arg	0
ATT	Ile	19	ACT	Thr	10	AAT	Asn	9	AGT	Ser	2
ATC	Ile	20	ACC	Thr	11	AAC	Asn	12	AGC	Ser	12
ATA	Ile	0	ACA	Thr	1	AAA	Lys	13	AGA	Arg	0
ATG	Met	11	ACG	Thr	0	AAG	Lys	22	AGG	Arg	0
GTT	Val	5	GCT	Ala	21	GAT	Asp	14	GGT	Gly	14
GTC	Val	26	GCC	Ala	12	GAC	Asp	12	GGC	Gly	21
GTA	Val	1	GCA	Ala	4	GAA	Glu	18	GGA	Gly	3
GTG	Val	17	GCG	Ala	0	GAG	Glu	20	GGG	Gly	1

Figure 6

Synthetic oligos for engineered GR/RD genes
(All oligos listed 5'to 3')

Coding strand: 5'____ _____(_____)n_____ ____3'
Non-coding strand: 3'_____ _____(_____)n_____ _5'

Oligos with pRAM flanking sequence identical for GR/RD
1) coding strand upstream flanking
RAM-C1: ACGCCAGCCCAAGCTTAGGCCTGAGTGGC   (SEQ ID NO:35)
RAM-C2: CTTAATTCTCCCCATCCCCCTGTTGACAATTAATCATCGGCTCG (SEQ ID NO:36)
RAM-C3: TATAATGTGAGGAATTGCGAGCGGATAACAATTTCACACA   (SEQ ID NO:37)

2) coding strand downstream flanking
RAM-C4: ATGGGATGTTACCTAGACCAATATGAAATATTTGGTAAAT   (SEQ ID NO:38)
RAM-C5: AAATGCTTAATGAATTTCAAAAAAAAAAAAAAAAGGAATTC   (SEQ ID NO:39)
RAM-C6: GATATCAAGCTTATCGATACCGTCGACCTCGAGGATTATA   (SEQ ID NO:40)
RAM-C7: TAGAAAAAGGCCTCGGCGGCCGCTAGTTCAGTCAGTT   (SEQ ID NO:41)

3) non-coding strand downstream flanking
RAM-N1: AACTGACTGAACTAGCG   (SEQ ID NO:42)
RAM-N2: GCCGCCGAGGCCTTTTTCTATATAATCCTCGAGGTCGACG   (SEQ ID NO:43)
RAM-N3: GTATCGATAAGCTTGATATCGAATTCCTTTTTTTTTTTTT   (SEQ ID NO:44)
RAM-N3b:AGCTTGATATCGAATTCCTTTTTTTTTTTTTTTTGAAATTC   (SEQ ID NO:45)
RAM-N4: TTGAAATTCATTAAGCATTTATTTACCAAATATTTCATAT   (SEQ ID NO:46)
RAM-N5: TGGTCTAGGTAACATCCCATCACTAGCTTTTTTTTCTATA   (SEQ ID NO:47)

4) non-coding strand upstream flanking
RAM-N6: TCGCAATTCCTCACATTATACGAGCCGATGATTAATTGTC   (SEQ ID NO:48)
RAM-N7: AACAGGGGGATGGGGAGAATTAAGGCCACTCAGGCCTAAGCTTGGGCTGGCGT
                                                      (SEQ ID NO:49)

GRver5 with flanking seq. of pRAM to end of *Sfi* I primers
1) Coding strand (Start and stop codons are underlined)
GR-C1: GGAAACAGGATCCC<u>ATGATG</u>AAACGCGAAAAGAACGTGAT   (SEQ ID NO:50)
GR-C2: CTACGGCCCAGAACCACTGCATCCACTGGAAGACCTCACC   (SEQ ID NO:51)
GR-C3: GCTGGTGAGATGCTCTTCCGAGCACTGCGTAAACATAGTC   (SEQ ID NO:52)
GR-C4: ACCTCCCTCAAGCACTCGTGGACGTCGTGGGAGACGAGAG   (SEQ ID NO:53)
GR-C5: CCTCTCCTACAAAGAATTTTTCGAAGCTACTGTGCTGTTG   (SEQ ID NO:54)
GR-C6: GCCCAAAGCCTCCATAATTGTGGGTACAAAATGAACGATG   (SEQ ID NO:55)
GR-C7: TGGTGAGCATTTGTGCTGAGAATAACACTCGCTTCTTTAT   (SEQ ID NO:56)
GR-C8: TCCTGTAATCGCTGCTTGGTACATCGGCATGATTGTCGCC   (SEQ ID NO:57)
GR-C9: CCTGTGAATGAATCTTACATCCCAGATGAGCTGTGTAAGG   (SEQ ID NO:58)
GR-C10: TTATGGGTATTAGCAAACCTCAAATCGTCTTTACTACCAA   (SEQ ID NO:59)
GR-C11: AAACATCTTGAATAAGGTCTTGGAAGTCCAGTCTCGTACT   (SEQ ID NO:60)
GR-C12: AACTTCATCAAACGCATCATTATTCTGGATACCGTCGAAA   (SEQ ID NO:61)
GR-C13: ACATCCACGGCTGTGAGAGCCTCCCTAACTTCATCTCTCG   (SEQ ID NO:62)
GR-C14: TTACAGCGATGGTAATATCGCTAATTTCAAGCCCTTGCAT   (SEQ ID NO:63)
GR-C15: TTTGATCCAGTCGAGCAAGTGGCCGCTATTTTGTGCTCCT   (SEQ ID NO:64)
GR-C16: CCGGCACCACTGGTTTGCCTAAAGGTGTCATGCAGACTCA   (SEQ ID NO:65)
GR-C17: CCAGAATATCTGTGTGCGTTTGATCCACGCTCTCGACCCT   (SEQ ID NO:66)
GR-C18: CGTGTGGGTACTCAATTGATCCCTGGCGTGACTGTGCTGG   (SEQ ID NO:67)
GR-C19: TGTATCTGCCTTTCTTTCACGCCTTTGGTTTCTCTATTAC   (SEQ ID NO:68)
GR-C20: CCTGGGCTATTTCATGGTCGGCTTGCGTGTCATCATGTTT   (SEQ ID NO:69)

Figure 6 (Cont.)

```
GR-C21:CGTCGCTTCGACCAAGAAGCCTTCTTGAAGGCTATTCAAG      (SEQ ID NO:70)
GR-C22:ACTACGAGGTGCGTTCCGTGATCAACGTCCCTTCAGTCAT      (SEQ ID NO:71)
GR-C23:TTTGTTCCTGAGCAAATCTCCTTTGGTTGACAAGTATGATCTG    (SEQ ID NO:72)
GR-C24:AGCAGCTTGCGTGAGCTGTGCTGTGGCGCTGCTCCTT         (SEQ ID NO:73)
GR-C25:TGGCCAAAGAAGTGGCCGAGGTCGCTGCTAAGCGTCTGAA      (SEQ ID NO:74)
GR-C26:CCTCCCTGGTATCCGCTGCGGTTTTGGTTTGACTGAGAGC      (SEQ ID NO:75)
GR-C27:ACTTCTGCTAACATCCATAGCTTGCGAGACGAGTTTAAGT      (SEQ ID NO:76)
GR-C28:CTGGTAGCCTGGGTCGCGTGACTCCTCTTATGGCTGCAAA      (SEQ ID NO:77)
GR-C29:GATCGCCGACCGTGAGACCGGCAAAGCACTGGGCCCAAAT      (SEQ ID NO:78)
GR-C30:CAAGTCGGTGAATTGTGTATTAAGGGCCCTATGGTCTCTA      (SEQ ID NO:79)
GR-C31:AAGGCTACGTGAACAATGTGGAGGCCACTAAAGAAGCCAT      (SEQ ID NO:80)
GR-C32:TGATGATGATGGCTGGCTCCATAGCGGCGACTTCGGTTAC      (SEQ ID NO:81)
GR-C33:TATGATGAGGACGAACACTTCTATGTGGTCGATCGCTACA      (SEQ ID NO:82)
GR-C34:AAGAATTGATTAAGTACAAAGGCTCTCAAGTCGCACCAGC      (SEQ ID NO:83)
GR-C35:CGAACTGGAAGAAATTTTGCTGAAGAACCCTTGTATCCGC      (SEQ ID NO:84)
GR-C36:GACGTGGCCGTCGTGGGTATCCCAGACTTGGAAGCTGGCG      (SEQ ID NO:85)
GR-C37:AGTTGCCTAGCGCCTTTGTGGTGAAACAACCCGGCAAGGA      (SEQ ID NO:86)
GR-C38:GATCACTGCTAAGGAGGTCTACGACTATTTGGCCGAGCGC      (SEQ ID NO:87)
GR-C39:GTGTCTCACACCAAATATCTGCGTGGCGGCGTCCGCTTCG      (SEQ ID NO:88)
GR-C40:TCGATTCTATTCCACGCAACGTTACCGGTAAGATCACTCG      (SEQ ID NO:89)
GR-C41:TAAAGAGTTGCTGAAGCAACTCCTCGAAAAAGCTGGCGGC      (SEQ ID NO:90)
GR-C42:TAGTAAAGTCTTCATGATTATATAGAAAAAAAAGCTAGTG      (SEQ ID NO:91)


2) non-coding strand
GR-N1:  TAATCATGAAGACTTTACTAGCCGCCAGCTTTTTCGAGGA     (SEQ ID NO:92)
GR-N2:  GTTGCTTCAGCAACTCTTTACGAGTGATCTTACCGGTAAC     (SEQ ID NO:93)
GR-N3:  GTTGCGTGGAATAGAATCGACGAAGCGGACGCCGCCACG      (SEQ ID NO:94)
GR-N4:  CAGATATTTGGTGTGAGACACGCGCTCGGCCAAATAGTCGT    (SEQ ID NO:95)
GR-N5:  AGACCTCCTTAGCAGTGATCTCCTTGCCGGGTTGTTTCAC     (SEQ ID NO:96)
GR-N6:  CACAAAGGCGCTAGGCAACTCGCCAGCTTCCAAGTCTGGG     (SEQ ID NO:97)
GR-N7:  ATACCCACGACGGCCACGTCGCGGATACAAGGGTTCTTCA     (SEQ ID NO:98)
GR-N8:  GCAAAATTTCTTCCAGTTCGGCTGGTGCGACTTGAGAGCC     (SEQ ID NO:99)
GR-N9:  TTTGTACTTAATCAATTCTTTGTAGCGATCGACCACATAG     (SEQ ID NO:100)
GR-N10:AAGTGTTCGTCCTCATCATAGTAACCGAAGTCGCCGCTAT      (SEQ ID NO:101)
GR-N11:GGAGCCAGCCATCATCATCAATGGCTTCTTTAGTGGCCTC      (SEQ ID NO:102)
GR-N12:CACATTGTTCACGTAGCCTTTAGAGACCATAGGGCCCTTA      (SEQ ID NO:103)
GR-N13:ATACACAATTCACCGACTTGATTTGGGCCCAGTGCTTTGC      (SEQ ID NO:104)
GR-N14:CGGTCTCACGGTCGGCGATCTTTGCAGCCATAAGAGGAGT      (SEQ ID NO:105)
GR-N15:CACGCGACCCAGGCTACCAGACTTAAACTCGTCTCGCAAG      (SEQ ID NO:106)
GR-N16:CTATGGATGTTAGCAGAAGTGCTCTCAGTCAAACCAAAAC      (SEQ ID NO:107)
GR-N17:CGCAGCGGATACCAGGGAGGTTCAGACGCTTAGCAGCGAC      (SEQ ID NO:108)
GR-N18:CTCGGCCACTTCTTTGGCCAAAGGAGCAGCGCCACAGCAC      (SEQ ID NO:109)
GR-N19:AGCTCACGCAAGCTGCTCAGATCATACTTGTCAACCAAAG      (SEQ ID NO:110)
GR-N20:GAGATTTGCTCAGGAACAAAATGACTGAAGGGACGTTGAT      (SEQ ID NO:111)
GR-N21:CACGGAACGCACCTCGTAGTCTTGAATAGCCTTCAA          (SEQ ID NO:112)
GR-N22:GAAGGCTTCTTGGTCGAAGCGACGAAACATGATGACACGCAAGC (SEQ ID NO:113)
GR-N23:CGACCATGAAATAGCCCAGGGTAATAGAGAAACCAAAGGC      (SEQ ID NO:114)
GR-N24:GTGAAAGAAAGGCAGATACACCAGCACAGTCACGCCAGGG      (SEQ ID NO:115)
GR-N25:ATCAATTGAGTACCCACACGAGGGTCGAGAGCGTGGATCA      (SEQ ID NO:116)
GR-N26:AACGCACACAGATATTCTGGTGAGTCTGCATGACACCTTT      (SEQ ID NO:117)
GR-N27:AGGCAAACCAGTGGTGCCGGAGGAGCACAAAATAGCGGCC      (SEQ ID NO:118)
```

Figure 6 (Cont.)

GR-N28:ACTTGCTCGACTGGATCAAAATGCAAGGGCTTGAAATTAG   (SEQ ID NO:119)
GR-N29:CGATATTACCATCGCTGTAACGAGAGATGAAGTTAGGGAG   (SEQ ID NO:120)
GR-N30:GCTCTCACAGCCGTGGATGTTTTCGACGGTATCCAGAATA   (SEQ ID NO:121)
GR-N31:ATGATGCGTTTGATGAAGTTAGTACGAGACTGGACTTCCA   (SEQ ID NO:122)
GR-N32:AGACCTTATTCAAGATGTTTTTGGTAGTAAAGACGATTTG   (SEQ ID NO:123)
GR-N33:AGGTTTGCTAATACCCATAACCTTACACAGCTCATCTGGG   (SEQ ID NO:124)
GR-N34:ATGTAAGATTCATTCACAGGGGCGACAATCATGCCGATGT   (SEQ ID NO:125)
GR-N35:ACCAAGCAGCGATTACAGGAATAAAGAAGCGAGTGTTATT   (SEQ ID NO:126)
GR-N36:CTCAGCACAAATGCTCACCACATCGTTCATTTTGTACCCA   (SEQ ID NO:127)
GR-N37:CAATTATGGAGGCTTTGGGCCAACAGCACAGTAGCTTCGA   (SEQ ID NO:128)
GR-N38:AAAATTCTTTGTAGGAGAGGCTCTCGTCTCCCACGACGTC   (SEQ ID NO:129)
GR-N39:CACGAGTGCTTGAGGGAGGTGACTATGTTTACGCAGTGCT   (SEQ ID NO:130)
GR-N40:CGGAAGAGCATCTCACCAGCGGTGAGGTCTTCCAGTGGAT   (SEQ ID NO:131)
GR-N41:GCAGTGGTTCTGGGCCGTAGATCACGTTCTTTTCGCGTTT   (SEQ ID NO:132)
GR-N42:<u>CATCAT</u>GGGATCCTGTTTCCTGTGTGAAATTGTTATCCGC   (SEQ ID NO:133)

RDver5 with flanking sequence of pRAM to end of *Sfi* I primers
1) coding strand
RD-C1: GGAAACAGGATCCC<u>ATGATG</u>AAGCGTGAGAAAAATGTCAT   (SEQ ID NO:134)
RD-C2: CTATGGCCCTGAGCCTCTCCATCCTTTGGAGGATTTGACT   (SEQ ID NO:135)
RD-C3: GCCGGCGAAATGCTGTTTCGTGCTCTCCGCAAGCACTCTC   (SEQ ID NO:136)
RD-C4: ATTTGCCTCAAGCCTTGGTCGATGTGGTCGGCGATGAATC   (SEQ ID NO:137)
RD-C5: TTTGAGCTACAAGGAGTTTTTTGAGGCAACCGTCTTGCTG   (SEQ ID NO:138)
RD-C6: GCTCAGTCCCTCCACAATTGTGGCTACAAGATGAACGACG   (SEQ ID NO:139)
RD-C7: TCGTTAGTATCTGTGCTGAAAACAATACCCGTTTCTTCAT   (SEQ ID NO:140)
RD-C8: TCCAGTCATCGCCGCATGGTATATCGGTATGATCGTGGCT   (SEQ ID NO:141)
RD-C9: CCAGTCAACGAGAGCTACATTCCCGACGAACTGTGTAAAG   (SEQ ID NO:142)
RD-C10:TCATGGGTATCTCTAAGCCACAGATTGTCTTCACCACTAA   (SEQ ID NO:143)
RD-C11:GAATATTCTGAACAAAGTCCTGGAAGTCCAAAGCCGCACC   (SEQ ID NO:144)
RD-C12:AACTTTATTAAGCGTATCATCATCTTGGACACTGTGGAGA   (SEQ ID NO:145)
RD-C13:ATATTCACGGTTGCGAATCTTTGCCTAATTTCATCTCTCG   (SEQ ID NO:146)
RD-C14:CTATTCAGACGGCAACATCGCAAACTTTAAACCACTCCAC   (SEQ ID NO:147)
RD-C15:TTCGACCCTGTGGAACAAGTTGCAGCCATTCTGTGTAGCA   (SEQ ID NO:148)
RD-C16:GCGGTACTACTGGACTCCCAAAGGGAGTCATGCAGACCCA   (SEQ ID NO:149)
RD-C17:TCAAAACATTTGCGTGCGTCTGATCCATGCTCTCGATCCA   (SEQ ID NO:150)
RD-C18:CGCTACGGCACTCAGCTGATTCCTGGTGTCACCGTCTTGG   (SEQ ID NO:151)
RD-C19:TCTACTTGCCTTTCTTCCATGCTTTCGGCTTTCATATTAC   (SEQ ID NO:152)
RD-C20:TTTGGGTTACTTTATGGTCGGTCTCCGCGTGATTATGTTC   (SEQ ID NO:153)
RD-C21:CGCCGTTTTGATCAGGAGGCTTTCTTGAAAGCCATCCAAG   (SEQ ID NO:154)
RD-C22:ATTATGAAGTCCGCAGTGTCATCAACGTGCCTAGCGTGAT   (SEQ ID NO:155)
RD-C23:CCTGTTTTTGTCTAAGAGCCCACTCGTGGACAAGTACGAC   (SEQ ID NO:156)
RD-C24:TTGTCTTCACTGCGTGAATTGTGTTGCGGTGCCGCTCCAC   (SEQ ID NO:157)
RD-C25:TGGCTAAGGAGGTCGCTGAAGTGGCCGCCAAACGCTTGAA   (SEQ ID NO:158)
RD-C26:TCTTCCAGGGATTCGTTGTGGCTTCGGCCTCACCGAATCT   (SEQ ID NO:159)
RD-C27:ACCAGCGCTATTATTCAGTCTCTCCGCGATGAGTTTAAGA   (SEQ ID NO:160)
RD-C28:GCGGCTCTTTGGGCCGTGTCACTCCACTCATGGCTGCTAA   (SEQ ID NO:161)
RD-C29:GATCGCTGATCGCGAAACTGGTAAGGCTTTGGGCCCTAAC   (SEQ ID NO:162)
RD-C30:CAAGTGGGCGAGCTGTGTATCAAAGGCCCTATGGTGAGCA   (SEQ ID NO:163)
RD-C31:AGGGTTATGTCAATAACGTCGAAGCTACCAAGGAGGCCAT   (SEQ ID NO:164)
RD-C32:CGACGACGACGGCTGGTTGCATTCTGGTGATTTTGGATAT   (SEQ ID NO:165)
RD-C33:TACGACGAAGATGAGCATTTTTACGTCGTGGATCGTTACA   (SEQ ID NO:166)
RD-C34:AGGAGCTGATCAAATACAAGGGTAGCCAGGTTGCTCCAGC   (SEQ ID NO:167)
RD-C35:TGAGTTGGAGGAGATTCTGTTGAAAAATCCATGCATTCGC   (SEQ ID NO:168)

Figure 6 (Cont.)

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RD-C36:GATGTCGCTGTGGTCGGCATTCCTGATCTGGAGGCCGGCG        (SEQ ID NO:169)
RD-C37:AACTGCCTTCTGCTTTCGTTGTCAAGCAGCCTGGTAAAGA        (SEQ ID NO:170)
RD-C38:AATTACCGCCAAAGAAGTGTATGATTACCTGGCTGAACGT        (SEQ ID NO:171)
RD-C39:GTGAGCCATACTAAGTACTTGCGTGGCGGCGTGCGTTTTG        (SEQ ID NO:172)
RD-C40:TTGACTCCATCCCTCGTAACGTAACAGGCAAAATTACCCG        (SEQ ID NO:173)
RD-C41:CAAGGAGCTGTTGAAACAATTGTTGGAGAAGGCCGGCGGT        (SEQ ID NO:174)
RD-C42:TAGTAAAGTCTTCATGATTATATAGAAAAAAAGCTAGTG         (SEQ ID NO:175)
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2) non-coding strand
```
RD-N1:  TAATCATGAAGACTTTACTAACCGCCGGCCTTCTCCAACA (SEQ ID NO:176)
RD-N2:  ATTGTTTCAACAGCTCCTTGCGGGTAATTTTGCCTGTTAC (SEQ ID NO:177)
RD-N3:  GTTACGAGGGATGGAGTCAACAAAACGCACGCCGCCACGC (SEQ ID NO:178)
RD-N4:  AAGTACTTAGTATGGCTCACACGTTCAGCCAGGTAATCAT (SEQ ID NO:179)
RD-N5:  ACACTTCTTTGGCGGTAATTTCTTTACCAGGCTGCTTGAC (SEQ ID NO:180)
RD-N6:  AACGAAAGCAGAAGGCAGTTCGCCGGCCTCCAGATCAGGA (SEQ ID NO:181)
RD-N7:  ATGCCGACCACAGCGACATCGCGAATGCATGGATTTTTCA (SEQ ID NO:182)
RD-N8:  ACAGAATCTCCTCCAACTCAGCTGGAGCAACCTGGCTACC (SEQ ID NO:183)
RD-N9:  CTTGTATTTGATCAGCTCCTTGTAACGATCCACGACGTAA (SEQ ID NO:184)
RD-N10:AAATGCTCATCTTCGTCGTAATATCCAAAATCACCAGAAT (SEQ ID NO:185)
RD-N11:GCAACCAGCCGTCGTCGTCGATGGCCTCCTTGGTAGCTTC (SEQ ID NO:186)
RD-N12:GACGTTATTGACATAACCCTTGCTCACCATAGGGCCTTTG (SEQ ID NO:187)
RD-N13:ATACACAGCTCGCCCACTTGGTTAGGGCCCAAAGCCTTAC (SEQ ID NO:188)
RD-N14:CAGTTTCGCGATCAGCGATCTTAGCAGCCATGAGTGGAGT (SEQ ID NO:189)
RD-N15:GACACGGCCCAAAGAGCCGCTCTTAAACTCATCGCGGAGA (SEQ ID NO:190)
RD-N16:GACTGAATAATAGCGCTGGTAGATTCGGTGAGGCCGA     (SEQ ID NO:191)
RD-N17:AGCCACAACGAATCCCTGGAAGATTCAAGCGTTTGGCGGCCAC (SEQ ID NO:192)
RD-N18:TTCAGCGACCTCCTTAGCCAGTGGAGCGGCACCGCAACAC (SEQ ID NO:193)
RD-N19:AATTCACGCAGTGAAGACAAGTCGTACTTGTCCACGAGTG (SEQ ID NO:194)
RD-N20:GGCTCTTAGACAAAAACAGGATCACGCTAGGCACGTTGAT (SEQ ID NO:195)
RD-N21:GACACTGCGGACTTCATAATCTTGGATGGCTTTCAAGAAA (SEQ ID NO:196)
RD-N22:GCCTCCTGATCAAAACGGCGGAACATAATCACGCGGAGAC (SEQ ID NO:197)
RD-N23:CGACCATAAAGTAACCCAAAGTAATATGAAAGCCGAAAGC (SEQ ID NO:198)
RD-N24:ATGGAAGAAAGGCAAGTAGACCAAGACGGTGACACCAGGA (SEQ ID NO:199)
RD-N25:ATCAGCTGAGTGCCGTAGCGTGGATCGAGAGCATGGATCA (SEQ ID NO:200)
RD-N26:GACGCACGCAAATGTTTTGATGGGTCTGCATGACTCCCTT (SEQ ID NO:201)
RD-N27:TGGGAGTCCAGTAGTACCGCTGCTACACAGAATGGCTGCA (SEQ ID NO:202)
RD-N28:ACTTGTTCCACAGGGTCGAAGTGGAGTGGTTTAAAGTTTG (SEQ ID NO:203)
RD-N29:CGATGTTGCCGTCTGAATAGCGAGAGATGAAATTAGGCAA (SEQ ID NO:204)
RD-N30:AGATTCGCAACCGTGAATATTCTCCACAGTGTCCAAGATG (SEQ ID NO:205)
RD-N31:ATGATACGCTTAATAAAGTTGGTGCGGCTTTGGACTTCCA (SEQ ID NO:206)
RD-N32:GGACTTTGTTCAGAATATTCTTAGTGGTGAAGACAATCTG (SEQ ID NO:207)
RD-N33:TGGCTTAGAGATACCCATGACTTTACACAGTTCGTCGGGA (SEQ ID NO:208)
RD-N34:ATGTAGCTCTCGTTGACTGGAGCCACGATCATACCGATAT (SEQ ID NO:209)
RD-N35:ACCATGCGGCGATGACTGGAATGAAGAAACGGGTATTGTT (SEQ ID NO:210)
RD-N36:TTCAGCACAGATACTAACGACGTCGTTCATCTTGTAGCCA (SEQ ID NO:211)
RD-N37:CAATTGTGGAGGGACTGAGCCAGCAAGACGGTTGCCTCAA (SEQ ID NO:212)
RD-N38:AAAACTCCTTGTAGCTCAAAGATTCATCGCCGACCACATC (SEQ ID NO:213)
RD-N39:GACCAAGGCTTGAGGCAAATGAGAGTGCTTGCGGAGAGCA (SEQ ID NO:214)
RD-N40:CGAAACAGCATTTCGCCGGCAGTCAAATCCTCCAAAGGAT (SEQ ID NO:215)
RD-N41:GGAGAGGCTCAGGGCCATAGATGACATTTTTCTCACGCTT (SEQ ID NO:216)
RD-N42:CATCATGGGATCCTGTTTCCTGTGTGAAATTGTTATCCGC (SEQ ID NO:217)
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Figure 7

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RELLUC.SEQ   A T G A C T T C ● A A G T T T A T G A T C C A G A A ● A G G A A A C G G A  40
RLUCVER1.SEQ A T G C T T C C A A G G T G T A C G A C C C C G A G C A G C G C A A G C G C A  40
RLUCVER2.SEQ A T G C T T C C A A G G T G T A C G A C C C C G A G C A A C G C A A A C G C A  40
RLUCFINL.SEQ A T G C T T C C A A G G T G T A C G A C C C C G A G C A A C G C A A A C G C A  40


RELLUC.SEQ   T G A T A A C T G G T C C G C A G T G G T G G G C C A G A T G T A A A C A A A T  80
RLUCVER1.SEQ T G A T C A C C G G C C C T C A G T G G T G G G C C C G C T G C A A G C A G A T  80
RLUCVER2.SEQ T G A T C A C T G G G C C T C A G T G G T G G G C T C G C T G C A A G C A A A T  80
RLUCFINL.SEQ T G A T C A C T G G G C C T C A G T G G T G G G C T C G C T G C A A G C A A A T  80


RELLUC.SEQ   G A A T G T T C T T G A T T C A T T T A T T A A T T A T T A T G A T T C A G A A  120
RLUCVER1.SEQ G A A C G T G C T G G A C T C C T T C A T C A A C T A C T A C G A C A G C G A G  120
RLUCVER2.SEQ G A A C G T G C T G G A C T C C T T C A T C A A C T A C T A T G A T T C C G A G  120
RLUCFINL.SEQ G A A C G T G C T G G A C T C C T T C A T C A A C T A C T A T G A T T C C G A G  120


RELLUC.SEQ   A A A C A T G C A G A A A A T G C T G T T A T T T T T T T A C A T G G T A A C G  160
RLUCVER1.SEQ A A G C A C G C C G A G A A C G C C G T G A T C T T C C T G C A C G G C A A C G  160
RLUCVER2.SEQ A A G C A C G C C G A G A A C G C C G T G A T T T T T C T G C A T G G T A A C G  160
RLUCFINL.SEQ A A G C A C G C C G A G A A C G C C G T G A T T T T T C T G C A T G G T A A C G  160


RELLUC.SEQ   C G G C C T C T T C T T A T T T A T G G C G A C A T G T T G T G C C A C A T A T  200
RLUCVER1.SEQ C C G C C T C C A G C T A C C T G T G G A G G C A C G T G G T G C C T C A C A T  200
RLUCVER2.SEQ C T G C C T C C A G C T A C C T G T G G A G G C A C G T C G T G C C T C A C A T  200
RLUCFINL.SEQ C T G C C T C C A G C T A C C T G T G G A G G C A C G T C G T G C C T C A C A T  200


RELLUC.SEQ   T G A G C C A G T A G C G C G G T G T A T T A T A C C A G A T C T T A T T G G T  240
RLUCVER1.SEQ C G A G C C C G T G G C C C G C T G C A T C A T C C C T G A C C T G A T C G G C  240
RLUCVER2.SEQ C G A G C C C G T G G C T C G C T G C A T C A T C C C T G A T C T G A T C G G A  240
RLUCFINL.SEQ C G A G C C C G T G G C T A G A T G C A T C A T C C C T G A T C T G A T C G G A  240


RELLUC.SEQ   A T G G G C A A A T C A G G C A A A T C T G G T A A T G G T T C T T A T A G G T  280
RLUCVER1.SEQ A T G G G C A A G T C C G G C A A G A G C G G C A A C G G C T C C T A C C G C C  280
RLUCVER2.SEQ A T G G G T A A G T C C G G C A A G A G C G G G A A T G G C T C A T A T C G C C  280
RLUCFINL.SEQ A T G G G T A A G T C C G G C A A G A G C G G G A A T G G C T C A T A T C G C C  280


RELLUC.SEQ   T A C T T G A T C A T T A C A A A T A T C T T A C T G C A T G G T T T G A A C T  320
RLUCVER1.SEQ T G C T G G A C C A C T A C A A G T A C C T G A C C G C C T G G T T C G A G C T  320
RLUCVER2.SEQ T C C T G G A T C A C T A C A A G T A C C T C A C C G C T T G G T T C G A G C T  320
RLUCFINL.SEQ T C C T G G A T C A C T A C A A G T A C C T C A C C G C T T G G T T C G A G C T  320


RELLUC.SEQ   T C T T A A T T T A C C A A A G A A G A T C A T T T T T G T C G G C C A T G A T  360
RLUCVER1.SEQ G C T G A A C C T G C C C A A G A A G A T C A T C T T C G T G G G C C A C G A C  360
RLUCVER2.SEQ G C T G A A C C T T C C A A A G A A A A T C A T C T T T G T G G G C C A C G A C  360
RLUCFINL.SEQ G C T G A A C C T T C C A A A G A A A A T C A T C T T T G T G G G C C A C G A C  360


RELLUC.SEQ   T G G G G T G C T T G T T T G G C A T T T C A T T A T A G C T A T G A G C A T C  400
RLUCVER1.SEQ T G G G G A G C C T G C C T G G C C T T C C A C T A C T C C T A C G A G C A C C  400
RLUCVER2.SEQ T G G G G G G C T T G T C T G G C C T T T C A C T A C T C C T A C G A G C A C C  400
RLUCFINL.SEQ T G G G G G G C T T G T C T G G C C T T T C A C T A C T C C T A C G A G C A C C  400


RELLUC.SEQ   A A G A T A A G A T C A A A G C A A T A G T T C A C G C T G A A A G T G T A G T  440
RLUCVER1.SEQ A G G A C A A G A T C A A G G C C A T C G T G C A C G C C G A G A G C G T G G T  440
RLUCVER2.SEQ A A G A C A A G A T C A A G G C C A T C G T C C A T G C T G A G A G T G T C G T  440
RLUCFINL.SEQ A A G A C A A G A T C A A G G C C A T C G T C C A T G C T G A G A G T G T C G T  440
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Figure 7 (Cont.)

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RELLUC.SEQ    A G A T G T G A T ● A A T C A T G G G A T G A A T G G ● T G A T A T T G A A  480
RLUCVER1.SEQ G G A C G T G A T C G A G T C C T G G G A C G A G T G G C C T G A C A T C G A G  480
RLUCVER2.SEQ G G A C G T G A T C G A G T C C T G G G A C G A G T G G C C T G A C A T C G A G  480
RLUCFINL.SEQ G G A C G T G A T C G A G T C C T G G G A C G A G T G G C C T G A C A T C G A G  480

RELLUC.SEQ    G A A G A T A T T G C G T T G A T C A A A T C T G A A G A A G G A G A A A A A A  520
RLUCVER1.SEQ G A G G A C A T C G C C C C T G A T C A A G A G C G A G G A G G G C G A G A A G A  520
RLUCVER2.SEQ G A G G A T A T C G C C C C T G A T C A A G A G C G A A G A G G G C G A G A A A A  520
RLUCFINL.SEQ G A G G A T A T C G C C C C T G A T C A A G A G C G A A G A G G G C G A G A A A A  520

RELLUC.SEQ    T G G T T T T G G A G A A T A A C T T C T T C G T G G A A A C C A T G T T G C C  560
RLUCVER1.SEQ T G G T G C T G G A G A A C A A C T T C T T C G T G G A G A C C A T G C T G C C  560
RLUCVER2.SEQ T G G T G C T T G A G A A T A A C T T C T T C G T C G A G A C C A T G C T C C C  560
RLUCFINL.SEQ T G G T G C T T G A G A A T A A C T T C T T C G T C G A G A C C A T G C T C C C  560

RELLUC.SEQ    A T C A A A A A T C A T G A G A A A G T T A G A A C C A G A A G A A T T T G C A  600
RLUCVER1.SEQ C A G C A A G A T C A T G C G C G C A A G C T G G A G C C T G A G G A G T T C G C C  600
RLUCVER2.SEQ A A G C A A G A T C A T G C G G A A A C T G G A G C C T G A G G A G T T C G C T  600
RLUCFINL.SEQ A A G C A A G A T C A T G C G G A A A C T G G A G C C T G A G G A G T T C G C T  600

RELLUC.SEQ    G C A T A T C T T G A A C C A T T C A A A G A G A A A G G T G A A G T T C G T C  640
RLUCVER1.SEQ G C C T A C C T G G A G C C C T T C A A G G A G A A G G G C G A G G T G C G C C  640
RLUCVER2.SEQ G C C T A C C T G G A G C C C T T C A A G G A G A A G G G C G A G G T T A G A C  640
RLUCFINL.SEQ G C C T A C C T G G A G C C A T T C A A G G A G A A G G G C G A G G T T A G A C  640

RELLUC.SEQ    G T C C A A C A T T A T C A T G G C C T C G T G A A A T C C C G T T A G T A A A  680
RLUCVER1.SEQ G C C C T A C C C T G T C C T G G C C C C G C G A G A T C C C T C T G G T G A A  680
RLUCVER2.SEQ G G C C T A C C C T C T C C T G G C C T C G C G A G A T C C C T C T C G T T A A  680
RLUCFINL.SEQ G G C C T A C C C T C T C C T G G C C T C G C G A G A T C C C T C T C G T T A A  680

RELLUC.SEQ    A G G T G G T A A A C C T G A C G T T G T A C A A A T T G T T A G G A A T T A T  720
RLUCVER1.SEQ G G G C G G C A A G C C C G A C G T G G T G C A G A T C G T G C G C A A C T A C  720
RLUCVER2.SEQ G G G A G G C A A G C C C G A C G T C G T C C A G A T T G T C C G C A A C T A C  720
RLUCFINL.SEQ G G G A G G C A A G C C C G A C G T C G T C C A G A T T G T C C G C A A C T A C  720

RELLUC.SEQ    A A T G C T T A T C T A C G T G C A A G T G A T G A T T T A C C A A A A A T G T  760
RLUCVER1.SEQ A A C G C C T A C C T G C G C G C C A G C G A C G A C C T G C C T A A G A T G T  760
RLUCVER2.SEQ A A C G C C T A C C T T C G G G C C A G C G A C G A T C T G C C T A A G A T G T  760
RLUCFINL.SEQ A A C G C C T A C C T T C G G G C C A G C G A C G A T C T G C C T A A G A T G T  760

RELLUC.SEQ    T T A T T G A A T C G G A T C C A G G A T T C T T T T C C A A T G C T A T T G T  800
RLUCVER1.SEQ T C A T C G A G T C C G A C C C T G G C T T C T T C T C C A A C G C C A T C G T  800
RLUCVER2.SEQ T C A T C G A G T C C G A C C C T G G G T T C T T T T C C A A C G C T A T T G T  800
RLUCFINL.SEQ T C A T C G A G T C C G A C C C T G G G T T C T T T T C C A A C G C T A T T G T  800

RELLUC.SEQ    T G A A G G C G C C A A G A A G T T T C C T A A T A C T G A A T T T G T C A A A  840
RLUCVER1.SEQ C G A G G G A G C C A A G A A G T T C C C C A A C A C C G A G T T C G T G A A G  840
RLUCVER2.SEQ C G A G G G A G C T A A G A A G T T C C C T A A C A C C G A G T T C G T G A A G  840
RLUCFINL.SEQ C G A G G G A G C T A A G A A G T T C C C T A A C A C C G A G T T C G T G A A G  840

RELLUC.SEQ    G T A A A A G G T C T T C A T T T T T T C G C A A G A A G A T G C A C C T G A T G  880
RLUCVER1.SEQ G T G A A G G G C C T G C A C T T C T C C C A G G A G G A C G C C C C T G A C G  880
RLUCVER2.SEQ G T G A A G G G C C T C C A C T T C A G C C A G G A G G A C G C T C C A G A T G  880
RLUCFINL.SEQ G T G A A G G G C C T C C A C T T T C A G C C A G G A G G A C G C T C C A G A T G  880
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Figure 7 (Cont.)

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RELLUC.SEQ    A A A T G G G A A   T A T A T C A A A T C G T T C G T   A G C G A G T T C T  920
RLUCVER1.SEQ A G A T G G G C A A G T A C A T C A A G A G C T T C G T G G A G C G C G T G C T  920
RLUCVER2.SEQ A A A T G G G T A A G T A C A T C A A G A G C T T C G T G G A G C G C G T G C T  920
RLUCFINL.SEQ A A A T G G G T A A G T A C A T C A A G A G C T T C G T G G A G C G C G T G C T  920


RELLUC.SEQ    C A A A A A T G A A C A A                                                      933
RLUCVER1.SEQ G A A G A A C G A G C A G                                                       933
RLUCVER2.SEQ G A A G A A C G A G C A G                                                       933
RLUCFINL.SEQ G A A G A A C G A G C A G                                                       933
```

Figure 8

```
RELLUC.SEQ   M T S K V Y D P ● R K R M I T G P Q W W A R C K Q M N ● D S F I N Y Y D S E  118
RLUCVER1.SEQ M A S K V Y D P E Q R K R M I T G P Q W W A R C K Q M N V L D S F I N Y Y D S E  118
RLUCVER2.SEQ M A S K V Y D P E Q R K R M I T G P Q W W A R C K Q M N V L D S F I N Y Y D S E  118
RLUCFINL.SEQ M A S K V Y D P E Q R K R M I T G P Q W W A R C K Q M N V L D S F I N Y Y D S E  118


RELLUC.SEQ   K H A E N A V I F L H G N A A S S Y L W R H V V P H I E P V A R C I I P D L I G  238
RLUCVER1.SEQ K H A E N A V I F L H G N A A S S Y L W R H V V P H I E P V A R C I I P D L I G  238
RLUCVER2.SEQ K H A E N A V I F L H G N A A S S Y L W R H V V P H I E P V A R C I I P D L I G  238
RLUCFINL.SEQ K H A E N A V I F L H G N A A S S Y L W R H V V P H I E P V A R C I I P D L I G  238


RELLUC.SEQ   M G K S G K S G N G S Y R L L D H Y K Y L T A W F E L L N L P K K I I F V G H D  358
RLUCVER1.SEQ M G K S G K S G N G S Y R L L D H Y K Y L T A W F E L L N L P K K I I F V G H D  358
RLUCVER2.SEQ M G K S G K S G N G S Y R L L D H Y K Y L T A W F E L L N L P K K I I F V G H D  358
RLUCFINL.SEQ M G K S G K S G N G S Y R L L D H Y K Y L T A W F E L L N L P K K I I F V G H D  358


RELLUC.SEQ   W G A C L A F H Y S Y E H Q D K I K A I V H A E S V V D V I E S W D E W P D I E  478
RLUCVER1.SEQ W G A C L A F H Y S Y E H Q D K I K A I V H A E S V V D V I E S W D E W P D I E  478
RLUCVER2.SEQ W G A C L A F H Y S Y E H Q D K I K A I V H A E S V V D V I E S W D E W P D I E  478
RLUCFINL.SEQ W G A C L A F H Y S Y E H Q D K I K A I V H A E S V V D V I E S W D E W P D I E  478


RELLUC.SEQ   E D I A L I K S E E G E K M V L E N N F F V E T M L P S K I M R K L E P E E F A  598
RLUCVER1.SEQ E D I A L I K S E E G E K M V L E N N F F V E T M L P S K I M R K L E P E E F A  598
RLUCVER2.SEQ E D I A L I K S E E G E K M V L E N N F F V E T M L P S K I M R K L E P E E F A  598
RLUCFINL.SEQ E D I A L I K S E E G E K M V L E N N F F V E T M L P S K I M R K L E P E E F A  598


RELLUC.SEQ   A Y L E P F K E K G E V R R P T L S W P R E I P L V K G G K P D V V Q I V R N Y  718
RLUCVER1.SEQ A Y L E P F K E K G E V R R P T L S W P R E I P L V K G G K P D V V Q I V R N Y  718
RLUCVER2.SEQ A Y L E P F K E K G E V R R P T L S W P R E I P L V K G G K P D V V Q I V R N Y  718
RLUCFINL.SEQ A Y L E P F K E K G E V R R P T L S W P R E I P L V K G G K P D V V Q I V R N Y  718


RELLUC.SEQ   N A Y L R A S D D L P K M F I E S D P G F F S N A I V E G A K K F P N T E F V K  838
RLUCVER1.SEQ N A Y L R A S D D L P K M F I E S D P G F F S N A I V E G A K K F P N T E F V K  838
RLUCVER2.SEQ N A Y L R A S D D L P K M F I E S D P G F F S N A I V E G A K K F P N T E F V K  838
RLUCFINL.SEQ N A Y L R A S D D L P K M F I E S D P G F F S N A I V E G A K K F P N T E F V K  838


RELLUC.SEQ   V K G L H F S Q E D A P D E M G K Y I K S F V E R V L K N E Q  931
RLUCVER1.SEQ V K G L H F S Q E D A P D E M G K Y I K S F V E R V L K N E Q  931
RLUCVER2.SEQ V K G L H F S Q E D A P D E M G K Y I K S F V E R V L K N E Q  931
RLUCFINL.SEQ V K G L H F S Q E D A P D E M G K Y I K S F V E R V L K N E Q  931
```

Figure 9A

Codon usage in RELLUC

(Renilla reniformis; Genbank ACCESSION:M63501; Medline:91239583)

TTT	Phe	11	TCT	Ser	5	TAT	Tyr	12	TGT	Cys	3
TTC	Phe	5	TCC	Ser	1	TAC	Tyr	1	TGC	Cys	0
TTA	Leu	8	TCA	Ser	6	TAA	***	0	TGA	***	0
TTG	Leu	4	TCG	Ser	4	TAG	***	0	TGG	Trp	8
CTT	Leu	8	CCT	Pro	5	CAT	His	9	CGT	Arg	4
CTC	Leu	1	CCC	Pro	0	CAC	His	1	CGC	Arg	0
CTA	Leu	1	CCA	Pro	11	CAA	Gln	6	CGA	Arg	2
CTG	Leu	0	CCG	Pro	2	CAG	Gln	1	CGG	Arg	2
ATT	Ile	12	ACT	Thr	4	AAT	Asn	11	AGT	Ser	2
ATC	Ile	6	ACC	Thr	1	AAC	Asn	2	AGC	Ser	1
ATA	Ile	3	ACA	Thr	1	AAA	Lys	21	AGA	Arg	2
ATG	Met	9	ACG	Thr	0	AAG	Lys	6	AGG	Arg	3
GTT	Val	12	GCT	Ala	5	GAT	Asp	16	GGT	Gly	10
GTC	Val	2	GCC	Ala	3	GAC	Asp	1	GGC	Gly	4
GTA	Val	6	GCA	Ala	8	GAA	Glu	25	GGA	Gly	3
GTG	Val	3	GCG	Ala	3	GAG	Glu	5	GGG	Gly	0

Figure 9B

Codon Usage in Rluc-final

TTT	Phe	4	TCT	Ser	0	TAT	Tyr	2	TGT	Cys	1
TTC	Phe	12	TCC	Ser	10	TAC	Tyr	11	TGC	Cys	2
TTA	Leu	0	TCA	Ser	1	TAA	***	0	TGA	***	0
TTG	Leu	0	TCG	Ser	0	TAG	***	0	TGG	Trp	8
CTT	Leu	3	CCT	Pro	11	CAT	His	2	CGT	Arg	0
CTC	Leu	6	CCC	Pro	3	CAC	His	8	CGC	Arg	7
CTA	Leu	0	CCA	Pro	4	CAA	Gln	3	CGA	Arg	0
CTG	Leu	13	CCG	Pro	0	CAG	Gln	4	CGG	Arg	3
ATT	Ile	3	ACT	Thr	1	AAT	Asn	2	AGT	Ser	1
ATC	Ile	18	ACC	Thr	4	AAC	Asn	11	AGC	Ser	7
ATA	Ile	0	ACA	Thr	0	AAA	Lys	4	AGA	Arg	2
ATG	Met	9	ACG	Thr	0	AAG	Lys	23	AGG	Arg	1
GTT	Val	2	GCT	Ala	11	GAT	Asp	6	GGT	Gly	3
GTC	Val	8	GCC	Ala	9	GAC	Asp	11	GGC	Gly	7
GTA	Val	0	GCA	Ala	0	GAA	Glu	2	GGA	Gly	3
GTG	Val	13	GCG	Ala	0	GAG	Glu	28	GGG	Gly	4

Figure 10

Oligonucleotides for the assembly of synthetic *Renilla* luciferase gene

Sense Strand

Oligo name	Oligo sequence from 5' to 3'	
RLS1 (1-40)	AACCATGGCTTCCAAGGTGTACGACCCCGAGCAACGCAAA	(SEQ ID NO:246)
RLS2 (41-80)	CGCATGATCACTGGGCCTCAGTGGTGGGCTCGCTGCAAGC	(SEQ ID NO:247)
RLS3 (81-120)	AAATGAACGTGCTGGACTCCTTCATCAACTACTATGATTC	(SEQ ID NO:248)
RLS4 (121-170)	CGAGAAGCACGCCGAGAACGCCGTGATTTTTCTGCATGGTAACGCTGCCT	
		(SEQ ID NO:249)
RLS5 (171-210)	CCAGCTACCTGTGGAGGCACGTCGTGCCTCACATCGAGCC	(SEQ ID NO:250)
RLS6 (211-250)	CGTGGCTAGATGCATCATCCCTGATCTGATCGGAATGGGT	(SEQ ID NO:251)
RLS7 (251-290)	AAGTCCGGCAAGAGCGGGAATGGCTCATATCGCCTCCTGG	(SEQ ID NO:252)
RLS8 (291-330)	ATCACTACAAGTACCTCACCGCTTGGTTCGAGCTGCTGAA	(SEQ ID NO:253)
RLS9 (331-370)	CCTTCCAAAGAAAATCATCTTTGTGGGCCACGACTGGGGG	(SEQ ID NO:254)
RLS10 (371-410)	GCTTGTCTGGCCTTTCACTACTCCTACGAGCACCAAGACA	(SEQ ID NO:255)
RLS11 (411-450)	AGATCAAGGCCATCGTCCATGCTGAGAGTGTCGTGGACGT	(SEQ ID NO:256)
RLS12 (451-495)	GATCGAGTCCTGGGACGAGTGGCCTGACATCGAGGAGGATATCGC	(SEQ ID NO:257)
RLS13 (496-535)	CCTGATCAAGAGCGAAGAGGGCGAGAAAATGGTGCTTGAG	(SEQ ID NO:258)
RLS14 (536-575)	AATAACTTCTTCGTCGAGACCATGCTCCCAAGCAAGATCA	(SEQ ID NO:259)
RLS15 (576-620)	TGCGGAAACTGGAGCCTGAGGAGTTCGCTGCCTACCTGGAGCCAT	(SEQ ID NO:260)
RLS16 (621-660)	TCAAGGAGAAGGGCGAGGTTAGACGGCCTACCCTCTCCTG	(SEQ ID NO:261)
RLS17 (661-700)	GCCTCGCGAGATCCCTCTCGTTAAGGGAGGCAAGCCCGAC	(SEQ ID NO:262)
RLS18 (701-740)	GTCGTCCAGATTGTCCGCAACTACAACGCCTACCTTCGGG	(SEQ ID NO:263)
RLS19 (741-780)	CCAGCGACGATCTGCCTAAGATGTTCATCGAGTCCGACCC	(SEQ ID NO:264)
RLS20 (781-820)	TGGGTTCTTTTCCAACGCTATTGTCGAGGGAGCTAAGAAG	(SEQ ID NO:265)
RLS21 (821-860)	TTCCCTAACACCGAGTTCGTGAAGGTGAAGGGCCTCCACT	(SEQ ID NO:266)
RLS22 (861-900)	TCAGCCAGGAGGACGCTCCAGATGAAATGGGTAAGTACAT	(SEQ ID NO:267)
RLS23 (901-949)	CAAGAGCTTCGTGGAGCGCGTGCTGAAGAACGAGCAGTAATTCTAGAGC	
		(SEQ ID NO:268)

Anti-sense Strand

Oligo name	Oligo Sequence from 5' to 3'	
RLAS1 (1-29)	GCTCTAGAATTACTGCTCGTTCTTCAGCA	(SEQ ID NO:269)
RLAS2 (30-69)	CGCGCTCCACGAAGCTCTTGATGTACTTACCCATTTCATC	(SEQ ID NO:270)
RLAS3 (70-109)	TGGAGCGTCCTCCTGGCTGAAGTGGAGGCCCTTCACCTTC	(SEQ ID NO:271)
RLAS4 (110-149)	ACGAACTCGGTGTTAGGGAACTTCTTAGCTCCCTCGACAA	(SEQ ID NO:272)
RLAS5 (150-189)	TAGCGTTGGAAAAGAACCCAGGGTCGGACTCGATGAACAT	(SEQ ID NO:273)
RLAS6 (190-229)	CTTAGGCAGATCGTCGCTGGCCCGAAGGTAGGCGTTGTAG	(SEQ ID NO:274)
RLAS7 (230-269)	TTGCGGACAATCTGGACGACGTCGGGCTTGCCTCCCTTAA	(SEQ ID NO:275)
RLAS8 (270-309)	CGAGAGGGATCTCGCGAGGCCAGGAGAGGGTAGGCCGTCT	(SEQ ID NO:276)
RLAS9 (310-349)	AACCTCGCCCTTCTCCTTGAATGGCTCCAGGTAGGCAGCG	(SEQ ID NO:277)
RLAS10 (350-394)	AACTCCTCAGGCTCCAGTTTCCGCATGATCTTGCTTGGGAGCATG	(SEQ ID NO:278)
RLAS11 (395-434)	GTCTCGACGAAGAAGTTATTCTCAAGCACCATTTTCTCGC	(SEQ ID NO:279)
RLAS12 (435-474)	CCTCTTCGCTCTTGATCAGGGCGATATCCTCCTCGATGTC	(SEQ ID NO:280)
RLAS13 (475-517)	AGGCCACTCGTCCCAGGACTCGATCACGTCCACGACACTCTCA	(SEQ ID NO:281)
RLAS14 (518-559)	GCATGGACGATGGCCTTGATCTTGTCTTGGTGCTCGTAGGAG	(SEQ ID NO:282)
RLAS15 (560-599)	TAGTGAAAGGCCAGACAAGCCCCCCAGTCGTGGCCCACAA	(SEQ ID NO:283)
RLAS16 (600-639)	AGATGATTTTCTTTGGAAGGTTCAGCAGCTCGAACCAAGC	(SEQ ID NO:284)
RLAS17 (640-679)	GGTGAGGTACTTGTAGTGATCCAGGAGGCGATATGAGCCA	(SEQ ID NO:285
RLAS18 (680-719)	TTCCCGCTCTTGCCGGACTTACCCATTCCGATCAGATCAG	(SEQ ID NO:286)
RLAS19 (720-764)	GGATGATGCATCTAGCCACGGGCTCGATGTGAGGCACGACGTGCC	(SEQ ID NO:287)
RLAS20 (765-804)	TCCACAGGTAGCTGGAGGCAGCGTTACCATGCAGAAAAAT	(SEQ ID NO:288)
RLAS21 (805-849)	CACGGCCGTTCTCGGCCGTGCTTCTCGGAATCATAGTAGTTGATGAA	(SEQ ID NO:289)
RLAS22 (850-889)	GGAGTCCAGCACGTTCATTTGCTTGCAGCGAGCCCACCAC	(SEQ ID NO:290)
RLAS23 (890-929)	TGAGGCCCAGTGATCATGCGTTTGCGTTGCTCGGGGTCGT	(SEQ ID NO:291)
RLAS24 (930-949)	ACACCTTGGAAGCCATGGTT	(SEQ ID NO:292)

Figure 11

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GRVER51.SEQ  A T G A T G A A ● G C G A A A A G A A C G T G A T C ● C G G C C A G A A C  40
LUCPPLYG.SEQ A T G A T G A A G A G A G A G A A A A A T G T T A T A T A T G G A C C C G A A C  40
RD1561H9.SEQ A T G A T A A A G C G T G A G A A A A A T G T C A T C T A T G G C C C T G A G C  40

GRVER51.SEQ  C A C T G C A T C C A C T G G A A G A C C T C A C C G C T G G T G A G A T G C T  80
LUCPPLYG.SEQ C C C T A C A C C C C T T G G A A G A C T T A A C A G C A G G A G A A A T G C T  80
RD1561H9.SEQ C T C T C C A T C C T T T G G A G G A T T T G A C T G C C G G C G A A A T G C T  80

GRVER51.SEQ  C T T C C G A G C A C T G C G T A A A C A T A G T C A C C T C C C T C A A G C A  120
LUCPPLYG.SEQ C T T C A G G G C C C T T C G A A A A C A T T C T C A T T T A C C G C A G G C T  120
RD1561H9.SEQ G T T T C G T G C T C T C C G C A A G C A C T C T C A T T T G C C T C A A G C C  120

GRVER51.SEQ  C T C G T G G A C G T C G T G G G A G A C G A G A G C C T C T C C T A C A A A G  160
LUCPPLYG.SEQ T T A G T A G A T G T G T T T G G T G A C G A A T C G C T T T C C T A T A A A G  160
RD1561H9.SEQ T T G G T C G A T G T G G T C G G C G A T G A A T C T T T G A G C T A C A A G G  160

GRVER51.SEQ  A A T T T T T C G A A G C T A C T G T G C T G T T G G C C C A A A G C C T C C A  200
LUCPPLYG.SEQ A G T T T T T T G A A G C T A C A T G C C T C C T A G C G C A A A G T C T C C A  200
RD1561H9.SEQ A G T T T T T T G A G G C A A C C G T C T T G C T G G C T C A G T C C C T C C A  200

GRVER51.SEQ  T A A T T G T G G G T A C A A A A T G A A C G A T G T G G T G A G C A T T T G T  240
LUCPPLYG.SEQ C A A T T G T G G A T A C A A G A T G A A T G A T G T A G T G T C G A T C T G C  240
RD1561H9.SEQ C A A T T G T G G C T A C A A G A T G A A C G A C G T C G T T A G T A T C T G T  240

GRVER51.SEQ  G C T G A G A A T A A C A C T C G C T T C T T T A T T C C T G T A A T C G C T G  280
LUCPPLYG.SEQ G C C G A G A A T A A T A A A A G A T T T T T T A T T C C C A T T A T T G C A G  280
RD1561H9.SEQ G C T G A A A A C A A T A C C C G T T T C T T C A T T C C A G T C A T C G C C G  280

GRVER51.SEQ  C T T G G T A C A T C G G C A T G A T T G T C G C C C C T G T G A A T G A A T C  320
LUCPPLYG.SEQ C T T G G T A T A T T G G T A T G A T T G T A G C A C C T G T T A A T G A A A G  320
RD1561H9.SEQ C A T G G T A T A T C G G T A T G A T C G T G G C C T C C A G T C A A C G A G A G  320

GRVER51.SEQ  T T A C A T C C C A G A T G A G C T G T G T A A G G T T A T G G G T A T T A G C  360
LUCPPLYG.SEQ T T A C A T C C C A G A T G A A C T C T G T A A G G T C A T G G G T A T A T C G  360
RD1561H9.SEQ C T A C A T T C C C G A C G A A C T G T G T A A A G T C A T G G G T A T C T C T  360

GRVER51.SEQ  A A A C C T C A A A T C G T C T T T A C T A C C A A A A A C A T C T T G A A T A  400
LUCPPLYG.SEQ A A A C C A C A A A T A G T T T T T T G T A C A A A G A A C A T T T T A A A T A  400
RD1561H9.SEQ A A G C C A C A G A T T G T C T T C A C C A C T A A G A A T A T T C T G A A C A  400

GRVER51.SEQ  A G G T C T T G G A A G T C C A G T C T C G T A C T A A C T T C A T C A A A C G  440
LUCPPLYG.SEQ A G G T A T T G G A G G T A C A G C A G A A C T A A T T T C A T A A A A A G  440
RD1561H9.SEQ A A G T C C T G G A A G T C C A A A G C C G C A C C A A C T T T A T T A A G C G  440

GRVER51.SEQ  C A T C A T T A T T C T G G A T A C C G T C G A A A A C A T C C A C G G C T G T  480
LUCPPLYG.SEQ G A T C A T C A T A C T T G A T A C T G T A G A A A A C A T A C A C G G T T G T  480
RD1561H9.SEQ T A T C A T C A T C T T G G A C A C T G T G G A G A A T A T T C A C G G T T G C  480

GRVER51.SEQ  G A G A G C C T C C C T A A C T T C A T C T C T C G T T A C A G C G A T G G T A  520
LUCPPLYG.SEQ G A A A G T C T T C C C A A T T T T A T T T C T C G T T A T T C G G A T G G A A  520
RD1561H9.SEQ G A A T C T T T G C C T A A T T T C A T C T C T C G C T A T T C A G A C G G C A  520

GRVER51.SEQ  A T A T C G C T A A T T T C A A G C C C T T G C A T T T T G A T C C A G T C G A  560
LUCPPLYG.SEQ A T A T T G C C A A C T T C A A A C C T T T A C A T T A C G A T C C T G T T G A  560
RD1561H9.SEQ A C A T C G C A A A C T T T A A A C C A C T C C A C T T C G A C C C T G T G G A  560
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Figure 11 (Cont.)

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GRVER51.SEQ   G C A A G T G G ● G C T A T T T T G T G C T C C T C ● C A C C A C T G G T   600
LUCPPLYG.SEQ  G C A A G T G G C A G C T A T C T T A T G T T C G T C A G G C A C T A C T G G A   600
RD1561H9.SEQ  A C A A G T T G C A G C C A T T C T G T G T A G C A G C G G T A C T A C T G G A   600

GRVER51.SEQ   T T G C C T A A A G G T G T C A T G C A G A C T C A C C A G A A T A T C T G T G   640
LUCPPLYG.SEQ  T T A C C G A A A G G T G T A A T G C A A A C T C A C C A A A A T A T T T G T G   640
RD1561H9.SEQ  C T C C C A A A G G G A G T C A T G C A G A C C C A T C A A A A C A T T T G C G   640

GRVER51.SEQ   T G C G T T T G A T C C A C G C T C T C G A C C C T C G T G T G G T A C T C A   680
LUCPPLYG.SEQ  T C C G A C T T A T A C A T G C T T T A G A C C C C A G G G C A G G A A C G C A   680
RD1561H9.SEQ  T G C G T C T G A T C C A T G C T C T C G A T C C A C G C T A C G G C A C T C A   680

GRVER51.SEQ   A T T G A T C C C T G G C G T G A C T G T G C T G G T G T A T C T G C C T T T C   720
LUCPPLYG.SEQ  A C T T A T T C C T G G T G T G A C A G T C T T A G T A T A T C T G C C T T T T   720
RD1561H9.SEQ  G C T G A T T C C T G G T G T C A C C G T C T T G G T C T A C T T G C C T T T C   720

GRVER51.SEQ   T T T C A C G C C T T T G G T T T C T C T A T T A C C C T G G G C T A T T C A   760
LUCPPLYG.SEQ  T T C C A T G C T T T T G G G T T C T C T A T A A A C T T G G G A T A T T C A   760
RD1561H9.SEQ  T T C C A T G C T T T C G G C T T T C A T A T T A C T T T G G G T T A C T T T A   760

GRVER51.SEQ   T G G T C G G C T T G C G T G T C A T C A T G T T T C G T C G C T T C G A C C A   800
LUCPPLYG.SEQ  T G G T G G G T C T T C G T G T T A T C A T G T T A A G A C G A T T T G A T C A   800
RD1561H9.SEQ  T G G T C G G T C T C C G C G T G A T T A T G T T C C G C C G T T T T G A T C A   800

GRVER51.SEQ   A G A A G C C T T C T T G A A G G C T A T T C A A G A C T A C G A G G T G C G T   840
LUCPPLYG.SEQ  A G A A G C A T T T C T A A A A G C T A T T C A G G A T T A T G A A G T T C G A   840
RD1561H9.SEQ  G G A G G C T T T C T T G A A A G C C A T C C A A G A T T A T G A A G T C C G C   840

GRVER51.SEQ   T C C G T G A T C A A C G T C C C T T C A G T C A T T T T G T T C C T G A G C A   880
LUCPPLYG.SEQ  A G T G T A A T T A A C G T T C C A G C A A T A A T A T T G T T C T T A T C G A   880
RD1561H9.SEQ  A G T G T C A T C A A C G T G C C T A G C G T G A T C C T G T T T T T G T C T A   880

GRVER51.SEQ   A A T C T C C T T T G G T T G A C A A G T A T G A T C T G A G C A G C T T G C G   920
LUCPPLYG.SEQ  A A A G T C C T T T G G T T G A C A A A T A C G A T T T A T C A A G T T T A A G   920
RD1561H9.SEQ  A G A G C C C A C T C G T G G A C A A G T A C G A C T T G T C T T C A C T G C G   920

GRVER51.SEQ   T G A G C T G T G C T G T G G G C G C T G C T C C T T T G G C C A A A G A A G T G   960
LUCPPLYG.SEQ  G G A A T T G T G T T G C G G T G C G G C A C C A T T A G C A A A A G A A G T T   960
RD1561H9.SEQ  T G A A T T G T G T T G C G G T G C C G C T C C A C T G G C T A A G A G G T C   960

GRVER51.SEQ   G C C G A G G T C G C T G C T A A G C G T C T G A A C C T C C C T G G T A T C C   1000
LUCPPLYG.SEQ  G C T G A G G T T G C A G T A A A A C G A T T A A A C T T G C C A G G A A T T C   1000
RD1561H9.SEQ  G C T G A A G T G G C C C G C C A A A C G C T T G A A T C T T C C A G G G A T T C   1000

GRVER51.SEQ   G C T G C G G T T T T G G T T T G A C T G A G A G C A C T T C T G C T A A C A T   1040
LUCPPLYG.SEQ  G C T G T G G A T T T G G T T T G A C A G A A T C T A C T T C A G C T A A T A T   1040
RD1561H9.SEQ  G G T G T G G C T T C G G C C T C A C C G A A T C T A C C A G T G C G A T T A T   1040

GRVER51.SEQ   C C A T A G C T T G C G A G A C G A G T T T A A G T C T G G T A G C C T G G G T   1080
LUCPPLYG.SEQ  A C A C A G T C T T G G G G A T G A A T T T A A A T C A G G A T C A C T T G G A   1080
RD1561H9.SEQ  C C A G A C T C T C G G G G A T G A G T T T A A G A G C G G C T C T T T G G G C   1080

GRVER51.SEQ   C G C G T G A C T C C T C T T A T G G C T G C A A A G A T C G C C G A C C G T G   1120
LUCPPLYG.SEQ  A G A G T T A C T C C T T T A A T G G C A G C T A A A A T A G C A G A T A G G G   1120
RD1561H9.SEQ  C G T G T C A C T C C A C T C A T G G C T G C T A A G A T C G C T G A T C G C C G   1120
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Figure 11 (Cont.)

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GRVER51.SEQ  A G A C C G G C ● A G C A C T G G G C C C A A A T C A ● T C G G T G A A T T  1160
LUCPPLYG.SEQ A A A C T G G T A A A G C A T T G G G A C C A A A T C A A G T T G G T G A A T T  1160
RD1561H9.SEQ A A A C T G G T A A G G C T T T G G G C C C G A A C C A A G T G G G C G A G C T  1160

GRVER51.SEQ  G T G T A T T A A G G G C C C T A T G G T C T C T A A A G G C T A C G T G A A C  1200
LUCPPLYG.SEQ A T G C G T T A A A G G T C C C A T G G T A T C G A A A G G T T A C G T G A A C  1200
RD1561H9.SEQ G T G T A T C A A A G G C C C T A T G G T G A G C A A G G G T T A T G T C A A T  1200

GRVER51.SEQ  A A T G T G G A G G C C A C T A A A G A A G C C A T T G A T G A T G A T G G C T  1240
LUCPPLYG.SEQ A A T G T A G A A G C T A C C A A A G A A G C T A T T G A T G A T G A T G G T T  1240
RD1561H9.SEQ A A C G T T G A A G C T A C C A A G G A G G C C A T C G A C G A C G A C G G C T  1240

GRVER51.SEQ  G G C T C C A T A G C G G C G A C T T C G G T T A C T A T G A T G A G G A C G A  1280
LUCPPLYG.SEQ G G C T T C A C T C T G G A G A C T T T G G A T A C T A T G A T G A G G A T G A  1280
RD1561H9.SEQ G G T G T T G C A T T C T G G T G A T T T T G G A T A T T A C G A C G A A G A T G A  1280

GRVER51.SEQ  A C A C T T C T A T G T G G T C G A T C G C T A C A A A G A A T T G A T T A A G  1320
LUCPPLYG.SEQ G C A T T T C T A T G T G G T G G A C C G T T A C A A G G A A T T G A T T A A A  1320
RD1561H9.SEQ G C A T T T T T A C G T C G T G G A T C G T T A C A A G G A G C T G A T C A A A  1320

GRVER51.SEQ  T A C A A A G G C T C T C A A G T C G C A C C A G C C G A A C T G G A A G A A A  1360
LUCPPLYG.SEQ T A T A A G G G C T C T C A G G T A G C A C C T G C A G A A C T A G A A G A G A  1360
RD1561H9.SEQ T A C A A G G G T A G C C A G G T T G C T C C A G C T G A G T T G G A G G A G A  1360

GRVER51.SEQ  T T T T G C T G A A G A A C C C T T G T A T C C C G C G A C G T G G C C G T C G T  1400
LUCPPLYG.SEQ T T T T A T T G A A A A A T C C A T G T A T C A G A G A T G T T G C T G T G G T  1400
RD1561H9.SEQ T T C T G T G T T G A A A A A T C C A T G C A T T C G C G A T G T C G C T G T G G T  1400

GRVER51.SEQ  G G G T A T C C C A G A C T T G G A A G C T G G C G A G T T G C C T A G C G C C  1440
LUCPPLYG.SEQ T G G T A T T C C T G A T C T A G A A G C T G G A G A A C T G C C A T C T G C G  1440
RD1561H9.SEQ C G G C A T T C C T G A T C T G G A G G C C G G C G A A C T G C C T T C T G C T  1440

GRVER51.SEQ  T T T G T G G T G A A A C A A C C C G G C A A G G A G A T C A C T G C T A A G G  1480
LUCPPLYG.SEQ T T T G T G G T T A A A C A G C C C G G A A A G G A G A T T A C A G C T A A A G  1480
RD1561H9.SEQ T T C G T T G T C A A G C A G C C T G G T A C A G A A T T A C C G C C A A A G  1480

GRVER51.SEQ  A G G T C T A C G A C T A T T T G G C C G A G C G C G T G T C T C A C A C C A A  1520
LUCPPLYG.SEQ A A G T G T A C G A T T A T C T T G C C G A G A G G G T C T C C C A T A C A A A  1520
RD1561H9.SEQ A A G T G T A T G A T T A C C T G G C T G A A C G T G T G A G C C A T A C T A A  1520

GRVER51.SEQ  A T A T C T G C G T G G C G G C G T C C G C T T C G T C G A T T C T A T T C C A  1560
LUCPPLYG.SEQ G T A T T T G C G T G G A G G G G G T T C G A T T C G T T G A T A G C A T A C C A  1560
RD1561H9.SEQ G T A C T T G C G T G G C G G C G T G C G T T T T G T T G A C T C C A T C C C T  1560

GRVER51.SEQ  C G C A A C G T T A C C G G T A A G A T C A C T C G T A A A G A G T T G C T G A  1600
LUCPPLYG.SEQ A G G A A T G T T A C A G G T A A A A T T A C A A G A A A G G A A C T T C T G A  1600
RD1561H9.SEQ C G T A A C G T A A C A G G C A A A A T T A C C C G C A A G G A G C T G T T G A  1600

GRVER51.SEQ  A G C A A C T C C T C G A A A A G C T G G C G G C                              1626
LUCPPLYG.SEQ A G C A G T T G C T G G A G A A G A G T T C T A A A C T T                        1629
RD1561H9.SEQ A C A A T T G T T G G T G A A G G C C G G C G G T                              1626
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Figure 12

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GRVER51.SEQ  M M K R E K N V ● G P E P L H P L E D L T A G E M L ● L R K H S H L P Q A  118
LUCPPLYG.SEQ M M K R E K N V I Y G P E P L H P L E D L T A G E M L F R A L R K H S H L P Q A  118
RD1561H9.SEQ M I K R E K N V I Y G P E P L H P L E D L T A G E M L F R A L R K H S H L P Q A  118


GRVER51.SEQ  L V D V V G D E S L S Y K E F F E A T V L L A Q S L H N C G Y K M N D V V S I C  238
LUCPPLYG.SEQ L V D V F G D E S L S Y K E F F E A T C L L A Q S L H N C G Y K M N D V V S I C  238
RD1561H9.SEQ L V D V V G D E S L S Y K E F F E A T V L L A Q S L H N C G Y K M N D V V S I C  238


GRVER51.SEQ  A E N N T R F F I P V I A A W Y I G M I V A P V N E S Y I P D E L C K V M G I S  358
LUCPPLYG.SEQ A E N N K R F F I P I I A A W Y I G M I V A P V N E S Y I P D E L C K V M G I S  358
RD1561H9.SEQ A E N N T R F F I P V I A A W Y I G M I V A P V N E S Y I P D E L C K V M G I S  358


GRVER51.SEQ  K P Q I V F T T K N I L N K V L E V Q S R T N F I K R I I I L D T V E N I H G C  478
LUCPPLYG.SEQ K P Q I V F C T K N I L N K V L E V Q S R T N F I K R I I I L D T V E N I H G C  478
RD1561H9.SEQ K P Q I V F T T K N I L N K V L E V Q S R T N F I K R I I I L D T V E N I H G C  478


GRVER51.SEQ  E S L P N F I S R Y S D G N I A N F K P L H F D P V E Q V A A I L C S S G T T G  598
LUCPPLYG.SEQ E S L P N F I S R Y S D G N I A N F K P L H Y D P V E Q V A A I L C S S G T T G  598
RD1561H9.SEQ E S L P N F I S R Y S D G N I A N F K P L H F D P V E Q V A A I L C S S G T T G  598


GRVER51.SEQ  L P K G V M Q T H Q N I C V R L I H A L D P R V G T Q L I P G V T V L V Y L P F  718
LUCPPLYG.SEQ L P K G V M Q T H Q N I C V R L I H A L D P R A G T Q L I P G V T V L V Y L P F  718
RD1561H9.SEQ L P K G V M Q T H Q N I C V R L I H A L D P R Y G T Q L I P G V T V L V Y L P F  718


GRVER51.SEQ  F H A F G F S I T L G Y F M V G L R V I M F R R F D Q E A F L K A I Q D Y E V R  838
LUCPPLYG.SEQ F H A F G F S I N L G Y F M V G L R V I M L R R F D Q E A F L K A I Q D Y E V R  838
RD1561H9.SEQ F H A F G F H I T L G Y F M V G L R V I M F R R F D Q E A F L K A I Q D Y E V R  838


GRVER51.SEQ  S V I N V P S V I L F L S K S P L V D K Y D L S S L R E L C C G A A P L A K E V  958
LUCPPLYG.SEQ S V I N V P A I I L F L S K S P L V D K Y D L S S L R E L C C G A A P L A K E V  958
RD1561H9.SEQ S V I N V P S V I L F L S K S P L V D K Y D L S S L R E L C C G A A P L A K E V  958


GRVER51.SEQ  A E V A A K R L N L P G I R C G F G L T E S T S A N I H S L R D E F K S G S L G  1078
LUCPPLYG.SEQ A E V A V K R L N L P G I R C G F G L T E S T S A N I H S L G D E F K S G S L G  1078
RD1561H9.SEQ A E V A A K R L N L P G I R C G F G L T E S T S A I I Q T L G D E F K S G S L G  1078


GRVER51.SEQ  R V T P L M A A K I A D R E T G K A L G P N Q V G E L C I K G P M V S K G Y V N  1198
LUCPPLYG.SEQ R V T P L M A A K I A D R E T G K A L G P N Q V G E L C V K G P M V S K G Y V N  1198
RD1561H9.SEQ R V T P L M A A K I A D R E T G K A L G P N Q V G E L C I K G P M V S K G Y V N  1198


GRVER51.SEQ  N V E A T K E A I D D D G W L H S G D F G Y Y D E D E H F Y V V D R Y K E L I K  1318
LUCPPLYG.SEQ N V E A T K E A I D D D G W L H S G D F G Y Y D E D E H F Y V V D R Y K E L I K  1318
RD1561H9.SEQ N V E A T K E A I D D D G W L H S G D F G Y Y D E D E H F Y V V D R Y K E L I K  1318


GRVER51.SEQ  Y K G S Q V A P A E L E E I L L K N P C I R D V A V V G I P D L E A G E L P S A  1438
LUCPPLYG.SEQ Y K G S Q V A P A E L E E I L L K N P C I R D V A V V G I P D L E A G E L P S A  1438
RD1561H9.SEQ Y K G S Q V A P A E L E E I L L K N P C I R D V A V V G I P D L E A G E L P S A  1438


GRVER51.SEQ  F V V K Q P G K E I T A K E V Y D Y L A E R V S H T K Y L R G G V R F V D S I P  1558
LUCPPLYG.SEQ F V V K Q P G K E I T A K E V Y D Y L A E R V S H T K Y L R G G V R F V D S I P  1558
RD1561H9.SEQ F V V K Q P G T E I T A K E V Y D Y L A E R V S H T K Y L R G G V R F V D S I P  1558


GRVER51.SEQ  R N V T G K I T R K E L L K Q L L E K A G G                                       1624
LUCPPLYG.SEQ R N V T G K I T R K E L L K Q L L E K S S K L                                     1627
RD1561H9.SEQ R N V T G K I T R K E L L K Q L L V K A G G                                       1624
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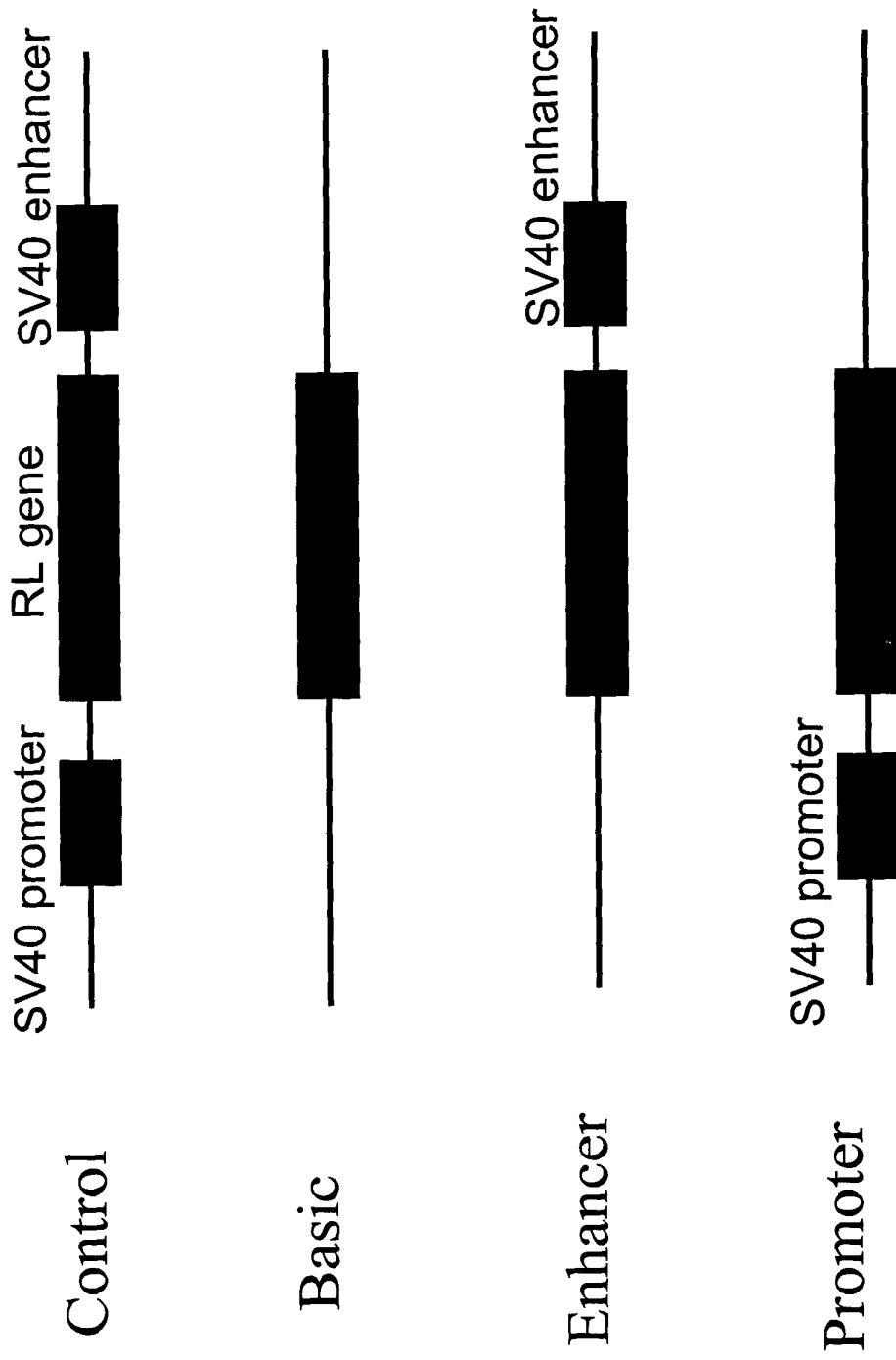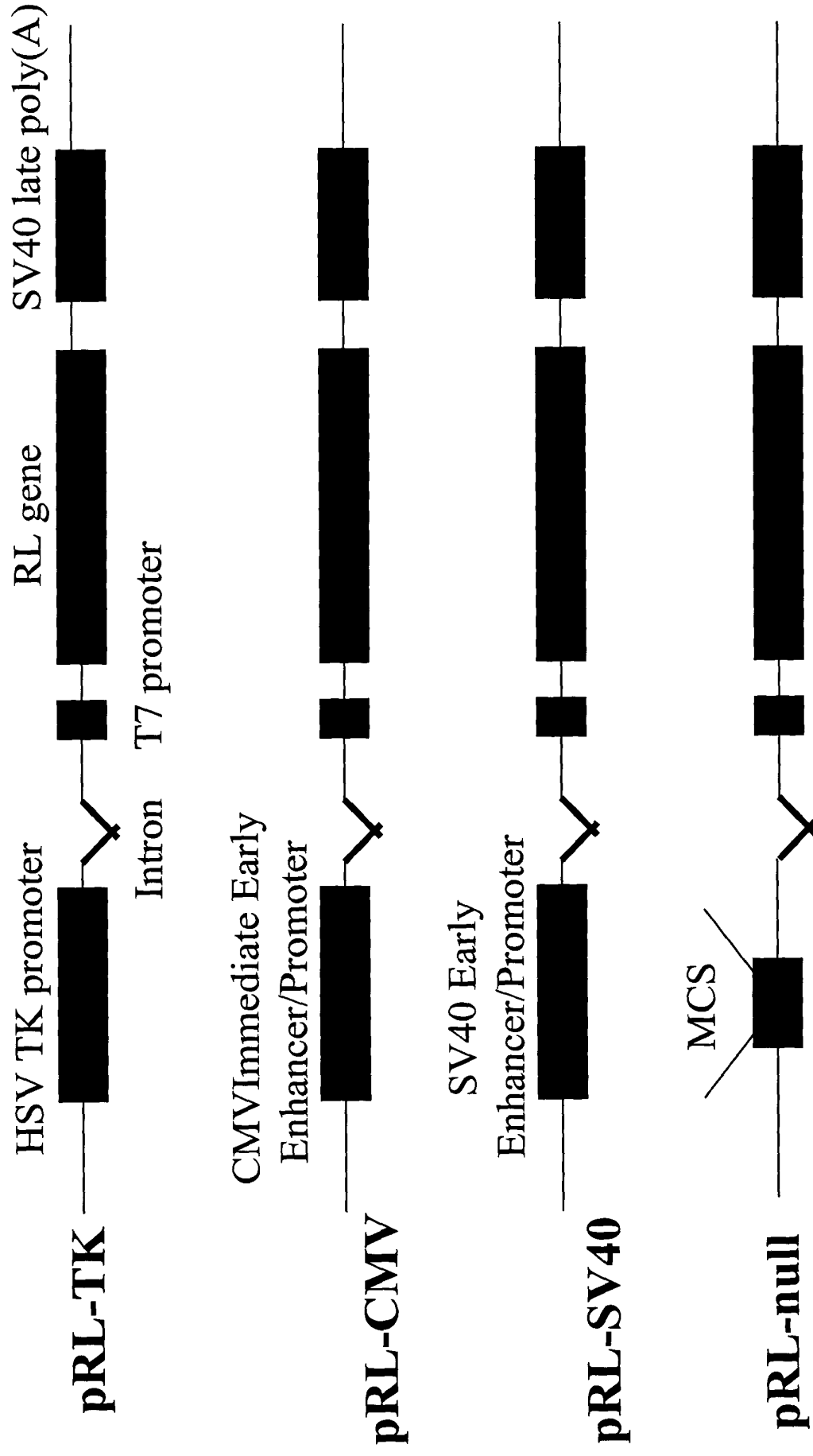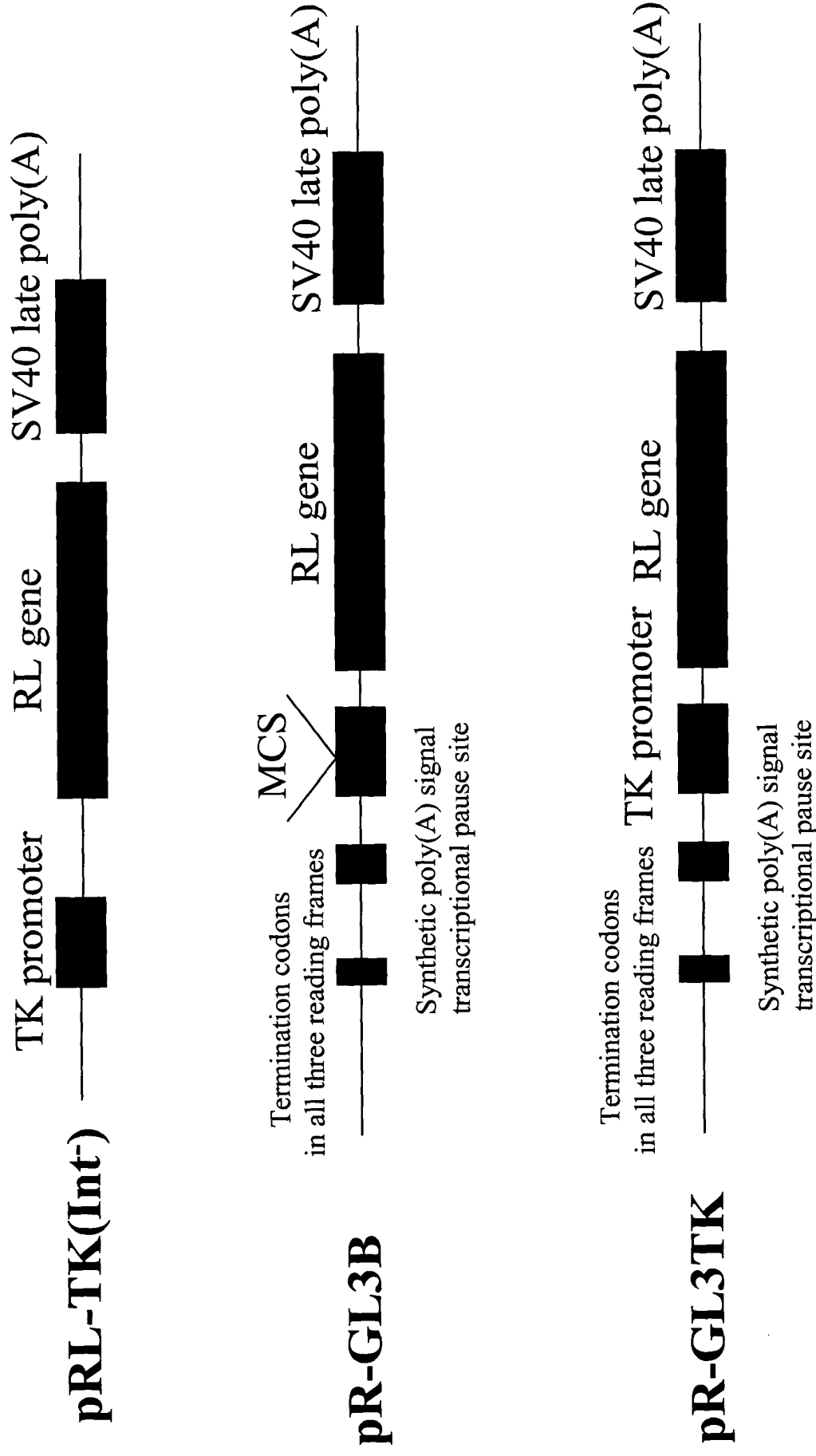
Renilla luciferease gene
in pGL3 series

Control   SV40 promoter   RL gene   SV40 enhancer

Basic

Enhancer   SV40 enhancer

Promoter   SV40 promoter

Fig 13A

Figure 13- RL Co-Reporter Vector Series

HSV TK promoter

RL gene

SV40 late poly(A)

Intron   T7 promoter

pRL-TK

CMV Immediate Early
Enhancer/Promoter

pRL-CMV

SV40 Early
Enhancer/Promoter

pRL-SV40

MCS

pRL-null

Figure 13 (Continued)

pRL-TK(Int⁻): TK promoter — RL gene — SV40 late poly(A)

pR-GL3B: Termination codons in all three reading frames — Synthetic poly(A) signal transcriptional pause site — MCS — RL gene — SV40 late poly(A)

pR-GL3TK: Termination codons in all three reading frames — Synthetic poly(A) signal transcriptional pause site — TK promoter — RL gene — SV40 late poly(A)

Halflife of RL-synthetic and RL-native in CHO Cells
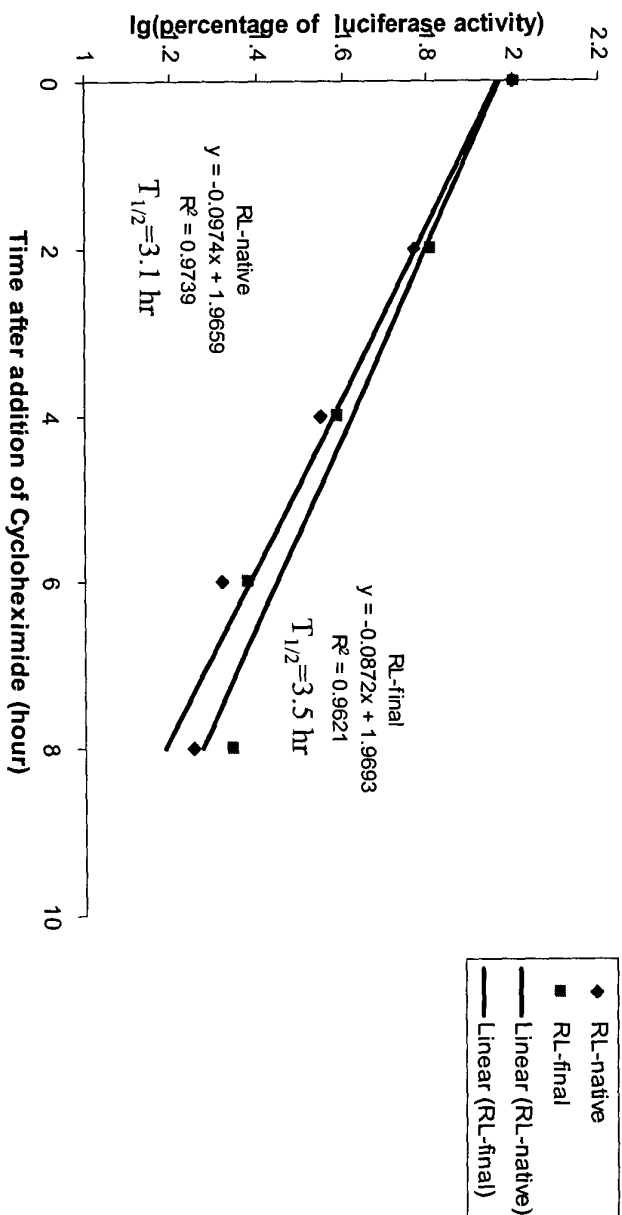
lg(percentage of luciferase activity)

RL-native
y = -0.0974x + 1.9659
R^2 = 0.9739
$T_{1/2}$=3.1 hr

RL-final
y = -0.0872x + 1.9693
R^2 = 0.9621
$T_{1/2}$=3.5 hr

Time after addition of Cycloheximide (hour)

◆ RL-native
■ RL-final
— Linear (RL-native)
— Linear (RL-final)

Fig 14

TNT (RL-final versus RL-native)

RLU

Reaction time (min)
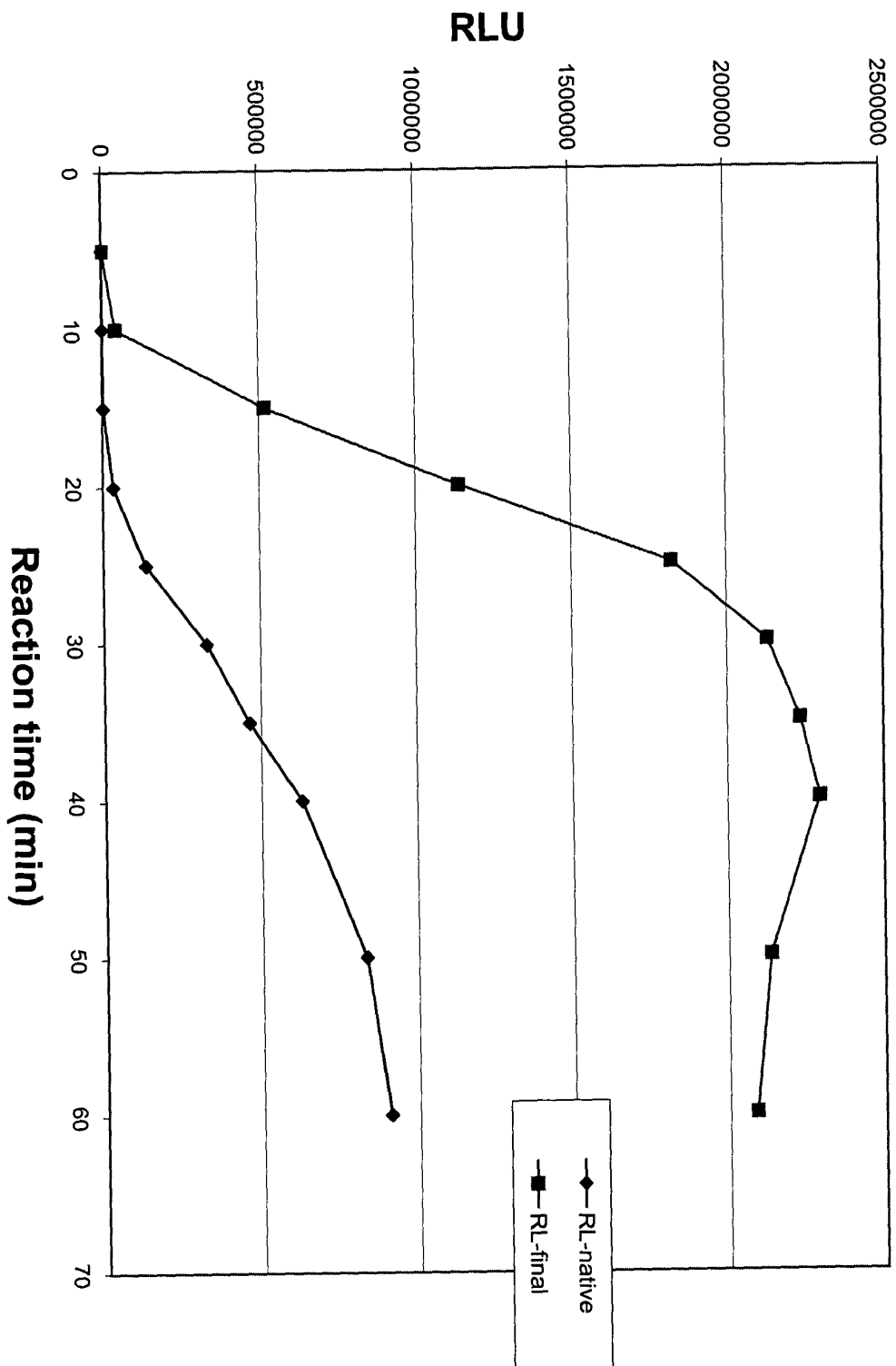
RL-native
RL-final

Fig 15A

TNT (RL-final versus RL-native, linear range)

y = 119195x - 1E+06
R² = 0.9938

y = 30467x - 596247
R² = 0.9938

RLU

Reaction time (minutes)
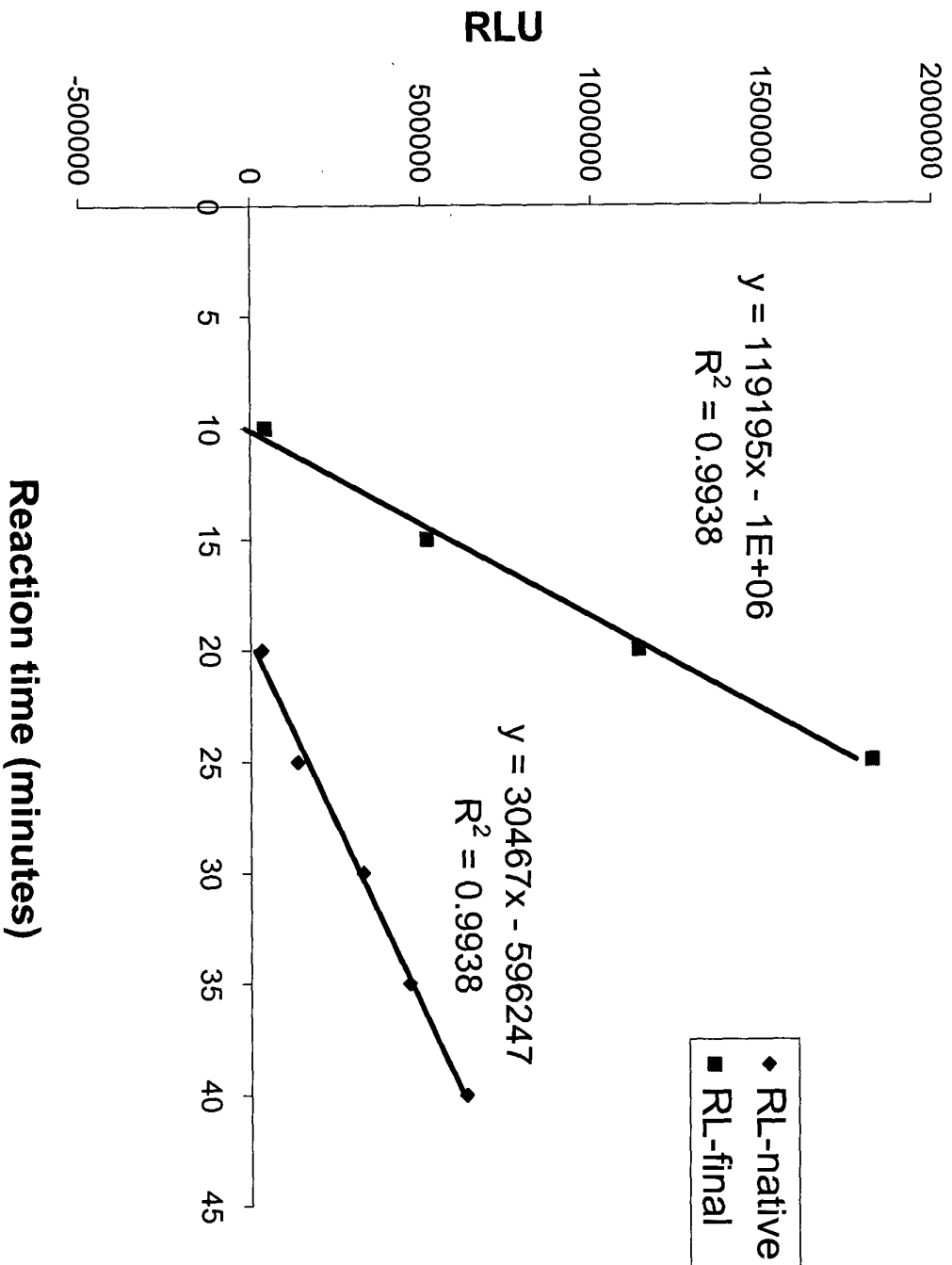
◆ RL-native
■ RL-final

Fig 15B

In vitro translation of RNAs of native RL and RL-final (30°C)
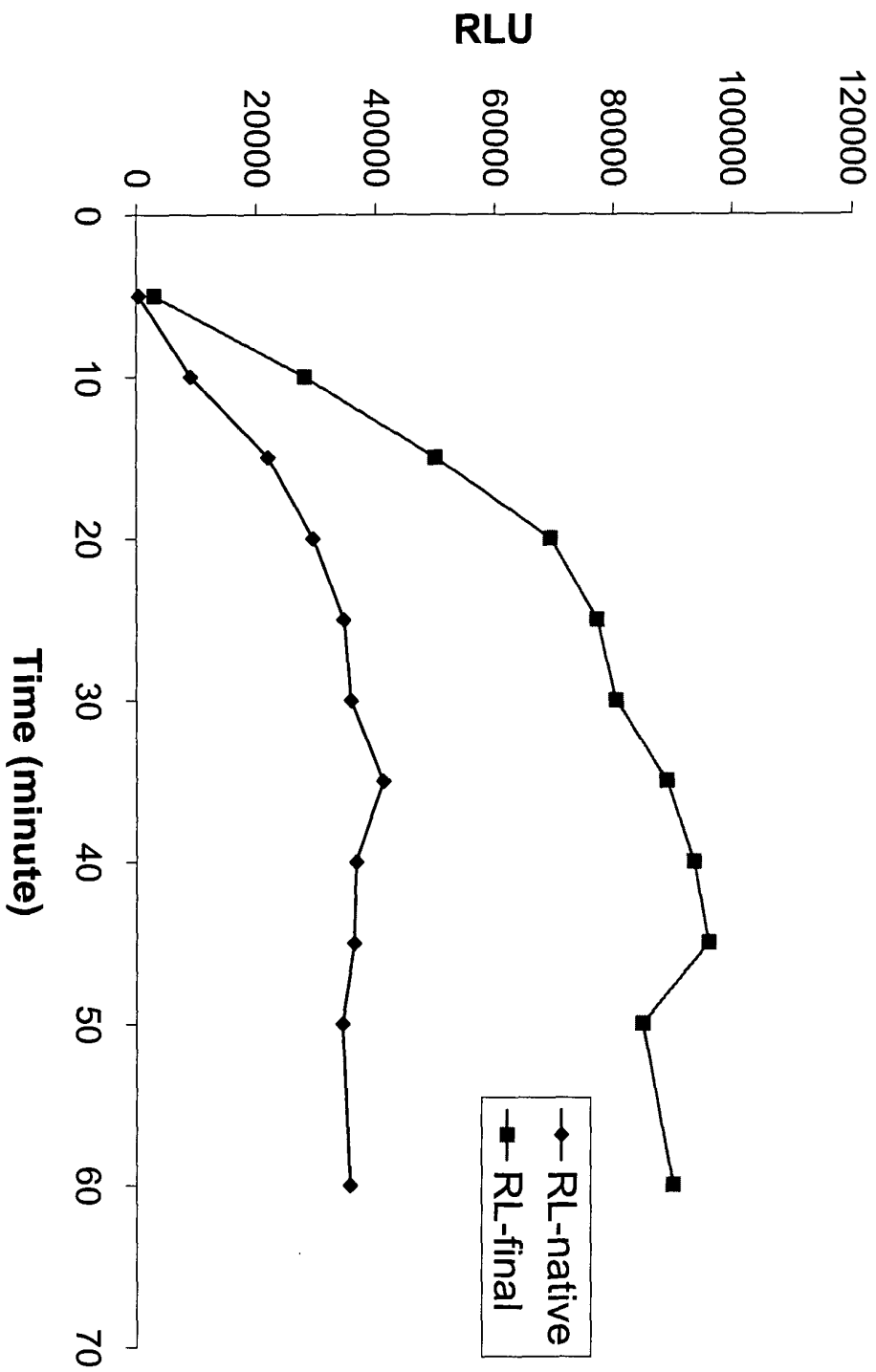
Fig 15C

In vitro translation of RNAs of native RL and RL-final
(30 °C, linear range)

y = 4426x - 17713
R² = 0.9969

y = 2001.2x - 9782.2
R² = 0.9902

RLU

Time (minute)

♦ RL-native
■ RL-final
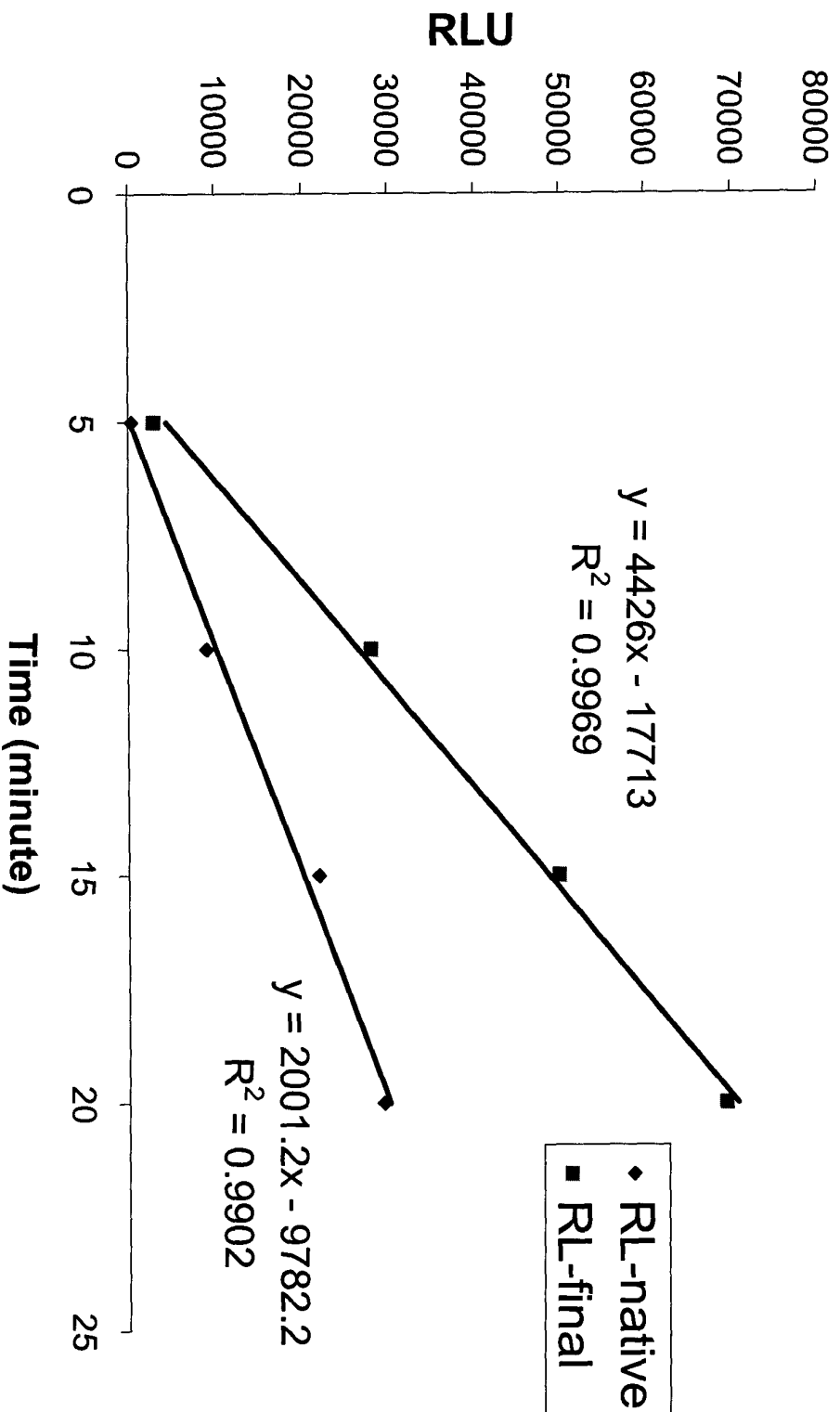
Fig 15D

In vitro translation using wheat germ extract

RLU

Time (min)

◆ RL-native
■ RL-final
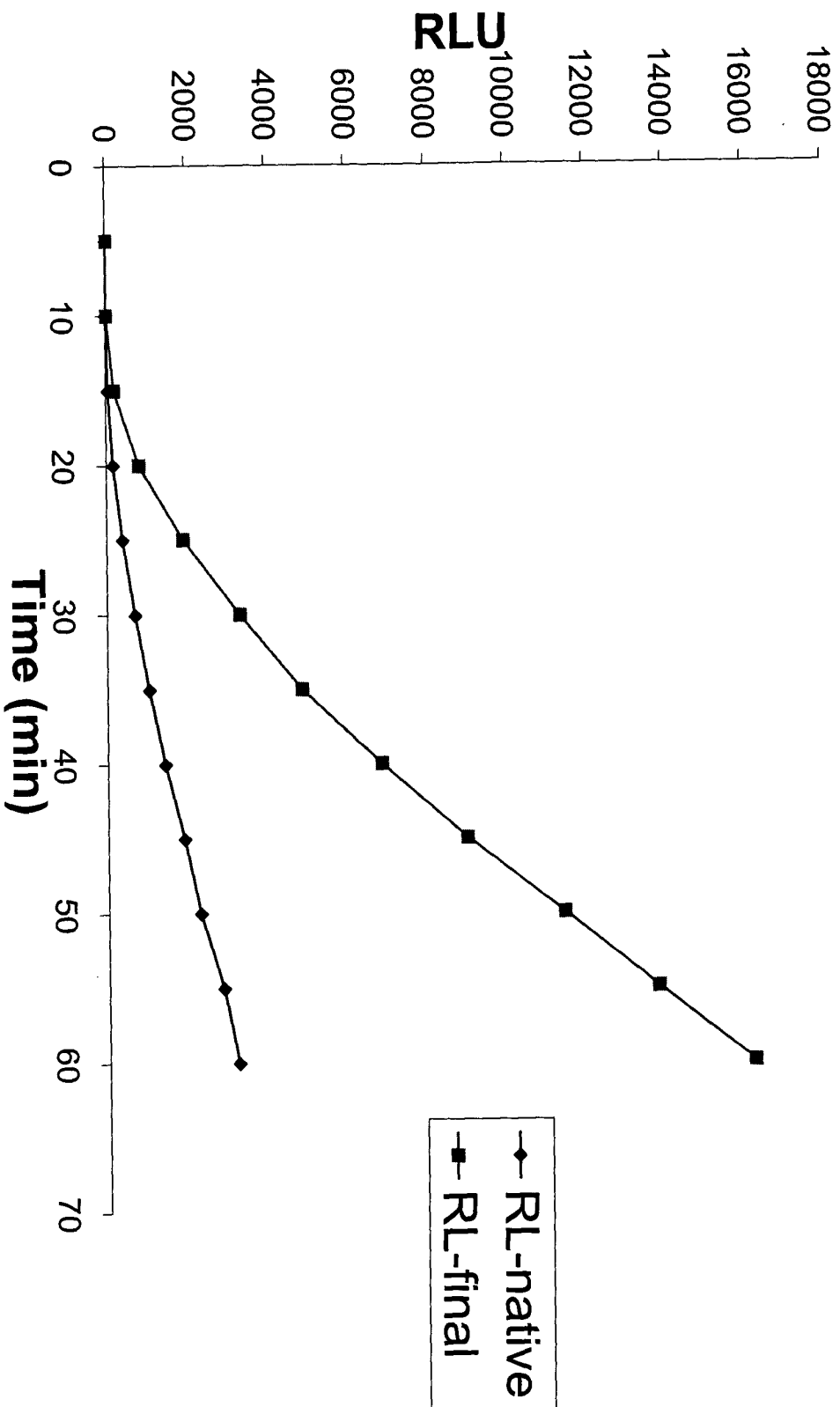
Fig 15E

In vitro translation using wheat germ extract
(linear range)

$y = 458.67x - 11393$
$R^2 = 0.9986$

$y = 89.467x - 2112.9$
$R^2 = 0.9974$

RLU

Time (min)

◆ RL-native
■ RL-final
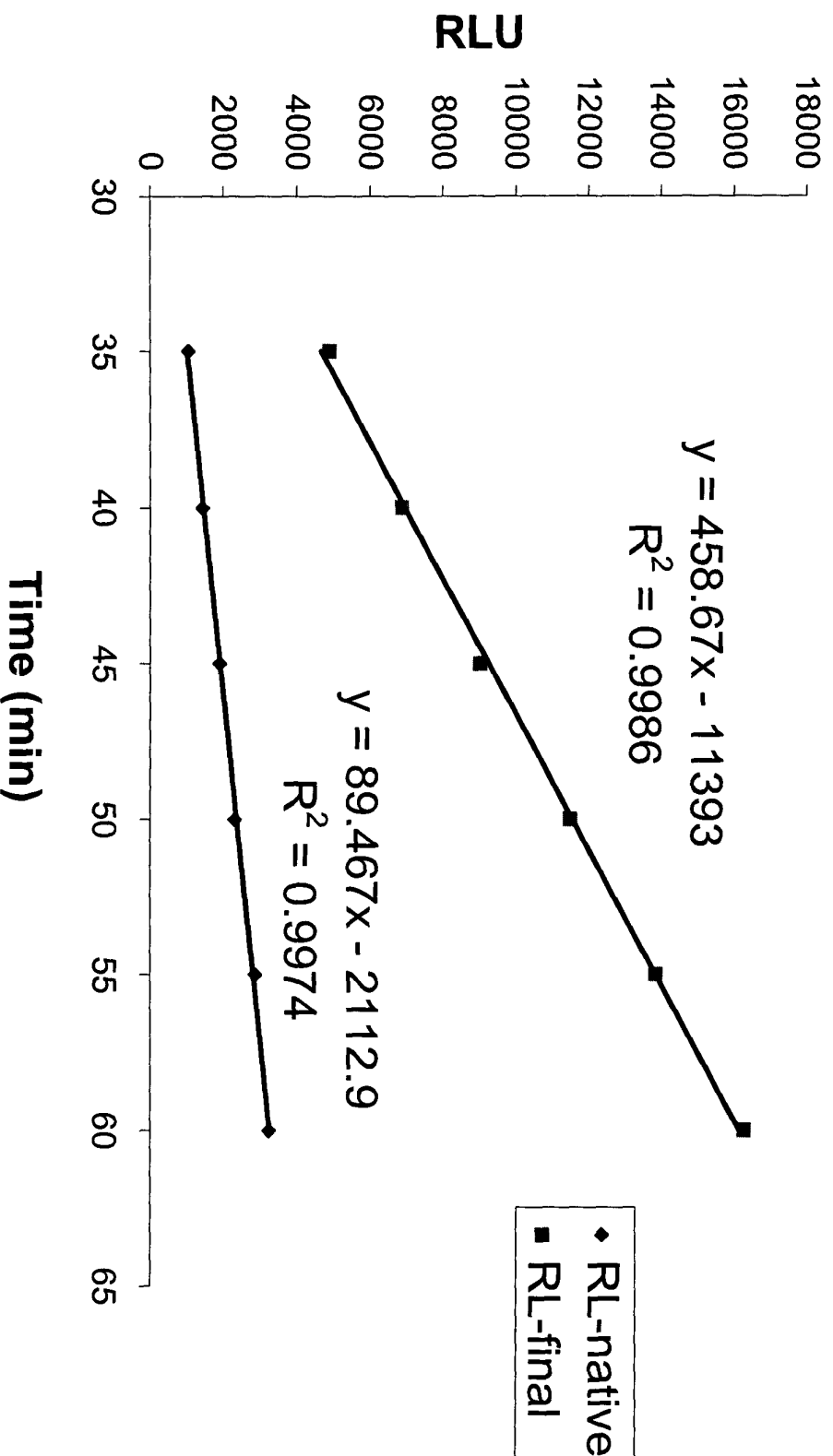
Fig 15F

Renilla expression
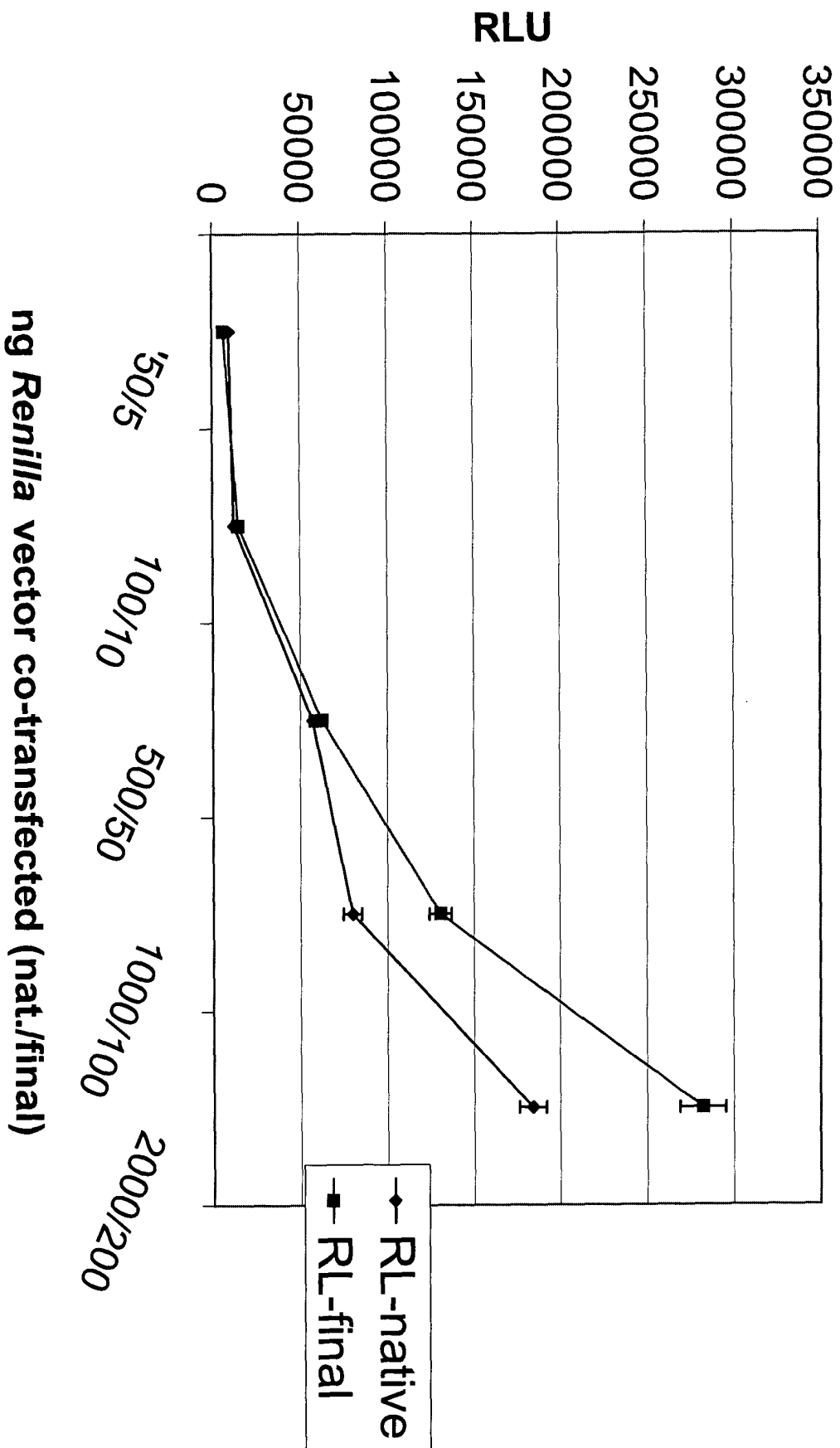
Fig 16A

Effect of firefly expression with increasing amounts of TK vector co-transfected

RLU

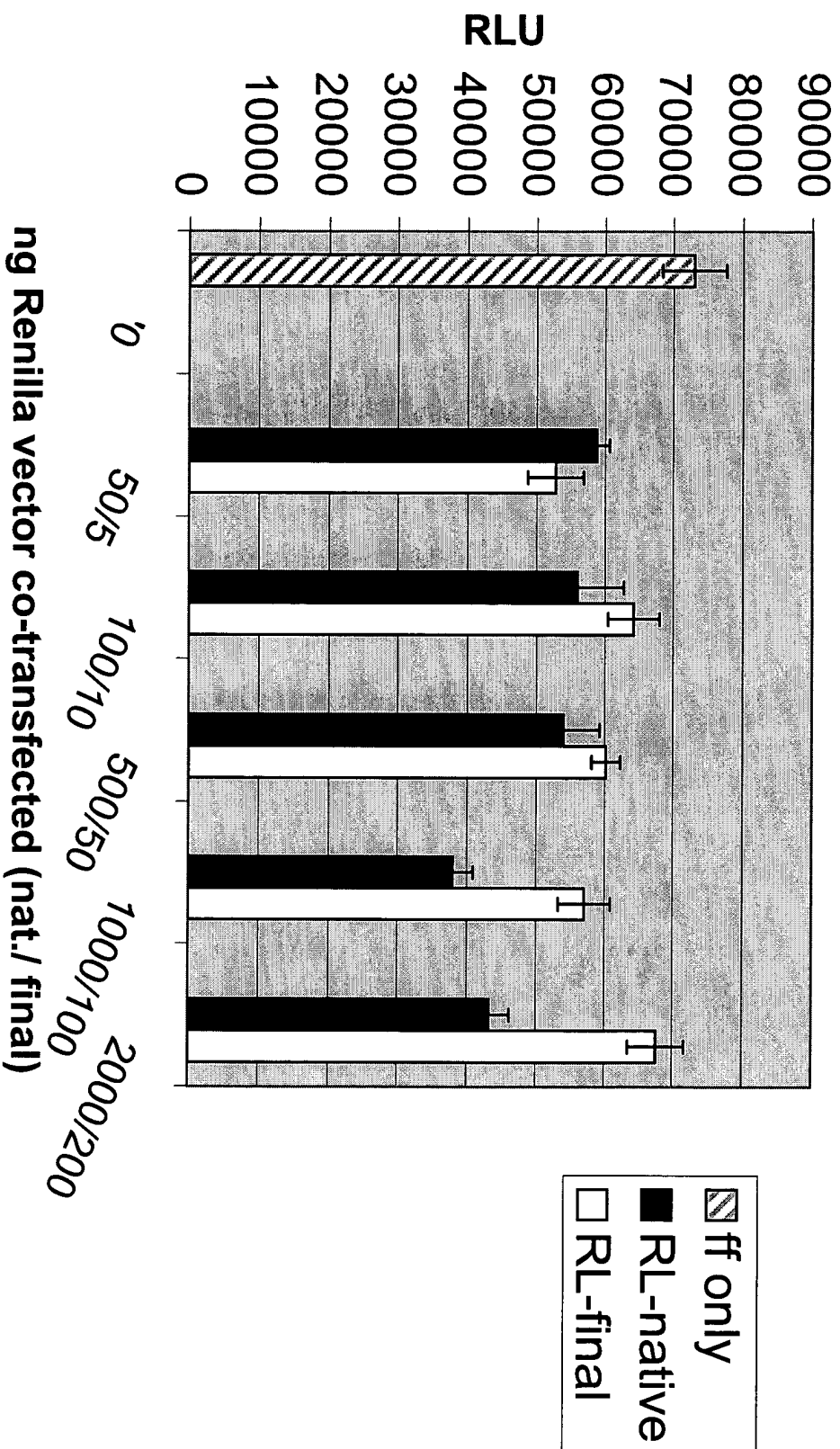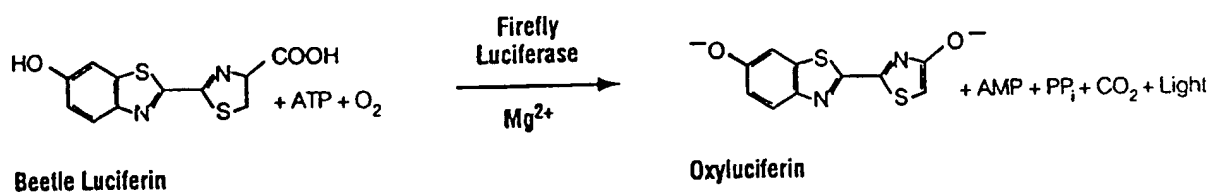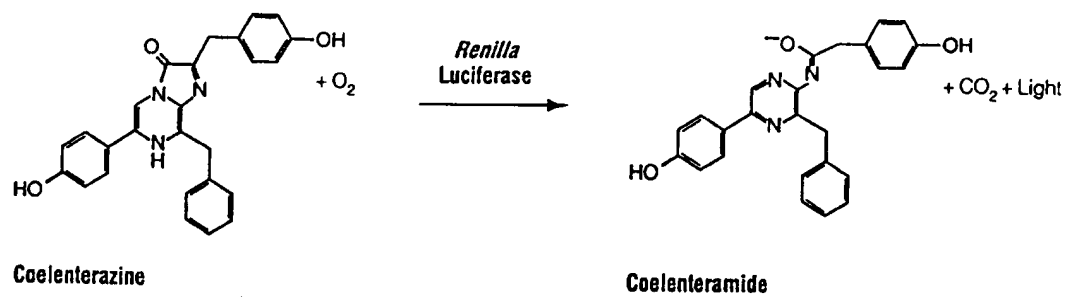ng Renilla vector co-transfected (nat./ final)

ff only
RL-native
RL-final

Fig 16B

Figure 17 A

Beetle Luciferin + ATP + O$_2$ → (Firefly Luciferase, Mg^{2+}) → **Oxyluciferin** + AMP + PP$_i$ + CO$_2$ + Light

Coelenterazine   Coelenteramide

Renilla Luciferase

$+ O_2$

$+ CO_2 + Light$

GRver5.1 DNA sequence of pGL3 vectors

```
ATGGTGAAACGCGAAAAGAACGTGATCTACGGCCCAGAACCACTGCATCC     50
ACTGGAAGACCTCACCGCTGGTGAGATGCTCTTCCGAGCACTGCGTAAAC    100
ATAGTCACCTCCCTCAAGCACTCGTGGACGTCGTGGGAGACGAGAgCCTC    150
TCCTACAAAGAATTTTTCGAAGCTACTGTGCTGTTGGCCCAAAGCCTCCA    200
TAATTGTGGGTACAAAATGAACGATGTGGTGAGCATTTGTGCTGAGAATA    250
ACACTCGCTTCTTTATTCCTGTAATCGCTGCTTGGTACATCGGCATGATT    300
GTCGCCCCTGTGAATGAATCTTACATCCCAGATGAGCTGTGTAAGGTTAT    350
GGGTATTAGCAAACCTCAAATCGTCTTTACTACCAAAAACATCTTGAATA    400
AGGTCTTGGAAGTCCAGTCTCGTACTAACTTCATCAAACGCATCATTATT    450
CTGGATACCGTCGAAAACATCCACGGCTGTGAGAGCCTCCCTAACTTCAT    500
CTCTCGTTACAGCGATGGTAATATCGCTAATTTCAAGCCCTTGCATTTTG    550
ATCCAGTCGAGCAAGTGGCCGCTATTTTGTGCTCCTCCGGCACCACTGGT    600
TTGCCTAAAGGTGTCATGCAGACTCACCAGAATATCTGTGTGCGTTTGAT    650
CCACGCTCTCGACCCTCGTGTGGGTACTCAATTGATCcCTGGCGTGACTG    700
TGCTGGTGTATCTGCCTTTCTTTCACGCCTTTGGTTTCTCTATTACCCTG    750
GGCTATTTCATGGTCGGCTTGCGTGTCATCATGTTTCGTCGCTTCGACCA    800
AGAAGCCTTCTTGAAGGCTATTCAAGACTACGAGGTGCGTTCCGTGATCA    850
ACGTCCCTTCAGTCATTTTGTTCCTGAGCAAATCTCCTTTGGTTGACAAG    900
TATGATCTGAGCAGCTTGCGTGAGCTGTGCTGTGGCGCTGCTCCTTTGGC    950
CAAAGAAGTGGCCGAGGTCGCTGCTAAGCGTCTGAACCTCCCTGGTATCC   1000
GCTGCGGTTTTGGTTTGACTGAGAGCACTTCTGCTAACATCCATAGCTTG   1050
CGAGACGAGTTTAAGTCTGGTAGCCTGGGTCGCGTGACTCCTCTTATGGC   1100
TGCAAAGATCGCCGACCGTGAGACCGGCAAAGCACTGGGCCCAAATCAAG   1150
TCGGTGAATTGTGTATTAAGGGCCCTATGGTCTCTAAAGGCTACGTGAAC   1200
AATGTGGAGGCCACTAAAGAAGCCATTGATGATGATGGCTGGCTCCATAG   1250
CGGCGACTTCGGTTACTATGATGAGGACGAACACTTCTATGTGGTCGATC   1300
GCTACAAAGAATTGATTAAGTACAAAGGCTCTCAAGTCGCACCAGCCGAA   1350
CTGGAAGAAATTTTGCTGAAGAACCCTTGTATCCGCGACGTGGCCGTCGT   1400
GGGTATCCCAGACTTGGAAGCTGGCGAGTTGCCTAGCGCCTTTGTGGTGA   1450
AACAACCCGGCAAGGAGATCACTGCTAAGGAGGTCTACGACTATTTGGCC   1500
GAGCGCGTGTCTCACACCAAATATCTGCGTGGCGGCGTCCGCTTCGTCGA   1550
TTCTATTCCACGCAACGTTACCGGTAAGATCACTCGTAAAGAGTTGCTGA   1600
AGCAACTCCTCGAAAAAGCTGGCGGC                           1626
```

SEQ ID NO: 297

Figure 18A

RDver5.1 DNA sequence of pGL3 vectors

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ATGGTGAAGCGTGAGAAAAATGTCATCTATGGCCCTGAGCCTCTCCATCC     50
TTTGGAGGATTTGACTGCCGGCGAAATGCTGTTTCGTGCTCTCCGCAAGC    100
ACTCTcATTTGCCTCAAGCCTTGGTCGATGTGGTCGGCGATGAATCTTTG    150
AGCTACAAGGAGTTTTTTGAGGCAACCGTCTTGCTGGCTCAGTCCCTCCA    200
CAATTGTGGCTACAAGATGAACGACGTCGTTAGTATCTGTGCTGAAAACA    250
ATACCCGTTTCTTCATTCCAGTCATCGCCGCATGGTATATCGGTATGATC    300
GTGGCTCCAGTCAACGAGAGCTACATTCCCGACGAACTGTGTAAAGTCAT    350
GGGTATCTCTAAGCCACAGATTGTCTTCACCACTAAGAATATTCTGAACA    400
AAGTCCTGGAAGTCCAAAGCCGCACCAACTTTATTAAGCGTATCATCATC    450
TTGGACACTGTGGAGAATATTCACGGTTGCGAATCTTTGCCTAATTTCAT    500
CTCTCGCTATTCAGACGGCAACATCGCAAACTTTAAACCACTCCACTTCG    550
ACCCTGTGGAACAAGTTGCAGCCATTCTGTGTAGCAGCGGTACTACTGGA    600
CTCCCAAAGGGAGTCATGCAGACCCATCAAAACATTTGCGTGCGTCTGAT    650
CCATGCTCTCGATCCACGCTACGGCACTCAGCTGATTCCTGGTGTCACCG    700
TCTTGGTCTACTTGCCTTTCTTCCATGCTTTCGGCTTTCATATTACTTTG    750
GGTTACTTTATGGTCGGTCTCCGCGTGATTATGTTCCGCCGTTTTGATCA    800
GGAGGCTTTCTTGAAAGCCATCCAAGATTATGAAGTCCGCAGTGTCATCA    850
ACGTGCCTAGCGTGATCCTGTTTTTGTCTAAGAGCCCACTCGTGGACAAG    900
TACGACTTGTCTTCACTGCGTGAATTGTGTTGCGGTGCCGCTCCACTGGC    950
TAAGGAGGTCGCTGAAGTGGCCGCCAAACGCTTGAATCTTCCAGGGATTC   1000
GTTGTGGCTTCGGCCTCACCGAATCTACCAGCGCTATTATTCAGTCTCTC   1050
CGCGATGAGTTTAAGAGCGGCTCTTTGGGCCGTGTCACTCCACTCATGGC   1100
TGCTAAGATCGCTGATCGCGAAACTGGTAAGGCTTTGGGCCCGAACCAAG   1150
TGGGCGAGCTGTGTATCAAAGGCCCTATGGTGAGCAAGGGTTATGTCAAT   1200
AACGTTGAAGCTACCAAGGAGGCCATCGACGACGACGGCTGGTTGCATTC   1250
TGGTGATTTTGGATATTACGACGAAGATGAGCATTTTTACGTCGTGGATC   1300
GTTACAAGGAGCTGATCAAATACAAGGGTAGCCAGGTTGCTCCAGCTGAG   1350
TTGGAGGAGATTCTGTTGAAAAAATCCATGCATTCGCGATGTCGCTGTGGT   1400
CGGCATTCCTGATCTGGAGGCCGGCGAACTGCCTTCTGCTTTCGTTGTCA   1450
AGCAGCCTGGTAAAGAAATTACCGCCAAAGAAGTGTATGATTACCTGGCT   1500
GAACGTGTGAGCCATACTAAGTACTTGCGTGGCGGCGTGCGTTTTGTTGA   1550
CTCCATCCCTCGTAACGTAACAGGCAAAATTACCCGCAAGGAGCTGTTGA   1600
AACAATTGTTGGAGAAGGCCGGCGGT                           1626
```

SEQ ID NO: 299

RD1561H9 DNA sequenc of pGL3 vectors

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ATGGTAAAGCGTGAGAAAAATGTCATCTATGGCCCTGAGCCTCTCCATCC     50
TTTGGAGGATTTGACTGCCGGCGAAATGCTGTTTCGTGCTCTCCGCAAGC    100
ACTCTCATTTGCCTCAAGCCTTGGTCGATGTGGTCGGCGATGAATCTTTG    150
AGCTACAAGGAGTTTTTTGAGGCAACCGTCTTGCTGGCTCAGTCCCTCCA    200
CAATTGTGGCTACAAGATGAACGACGTCGTTAGTATCTGTGCTGAAAACA    250
ATACCCGTTTCTTCATTCCAGTCATCGCCGCATGGTATATCGGTATGATC    300
GTGGCTCCAGTCAACGAGAGCTACATTCCCGACGAACTGTGTAAAGTCAT    350
GGGTATCTCTAAGCCACAGATTGTCTTCACCACTAAGAATATTCTGAACA    400
AAGTCCTGGAAGTCCAAAGCCGCACCAACTTTATTAAGCGTATCATCATC    450
TTGGACACTGTGGAGAATATTCACGGTTGCGAATCTTTGCCTAATTTCAT    500
CTCTCGCTATTCAGACGGCAACATCGCAAACTTTAAACCACTCCACTTCG    550
ACCCTGTGGAACAAGTTGCAGCCATTCTGTGTAGCAGCGGTACTACTGGA    600
CTCCCAAAGGGAGTCATGCAGACCCATCAAAACATTTGCGTGCGTCTGAT    650
CCATGCTCTCGATCCACGCTACGGCACTCAGCTGATTCCTGGTGTCACCG    700
TCTTGGTCTACTTGCCTTTCTTCCATGCTTTCGGCTTTCATATTACTTTG    750
GGTTACTTTATGGTCGGTCTCCGCGTGATTATGTTCCGCCGTTTTGATCA    800
GGAGGCTTTCTTGAAAGCCATCCAAGATTATGAAGTCCGCAGTGTCATCA    850
ACGTGCCTAGCGTGATCCTGTTTTTGTCTAAGAGCCCACTCGTGGACAAG    900
TACGACTTGTCTTCACTGCGTGAATTGTGTTGCGGTGCCGCTCCACTGGC    950
TAAGGAGGTCGCTGAAGTGGCCGCCAAACGCTTGAATCTTCCAGGGATTC   1000
GTTGTGGCTTCGGCCTCACCGAATCTACCAGTGCGATTATCCAGACTCTC   1050
GGGGATGAGTTTAAGAGCGGCTCTTTGGGCCGTGTCACTCCACTCATGGC   1100
TGCTAAGATCGCTGATCGCGAAACTGGTAAGGCTTTGGGCCCGAACCAAG   1150
TGGGCGAGCTGTGTATCAAAGGCCCTATGGTGAGCAAGGGTTATGTCAAT   1200
AACGTTGAAGCTACCAAGGAGGCCATCGACGACGACGGCTGGTTGCATTC   1250
TGGTGATTTTGGATATTACGACGAAGATGAGCATTTTTACGTCGTGGATC   1300
GTTACAAGGAGCTGATCAAATACAAGGGTAGCCAGGTTGCTCCAGCTGAG   1350
TTGGAGGAGATTCTGTTGAAAAATCCATGCATTCGCGATGTCGCTGTGGT   1400
CGGCATTCCTGATCTGGAGGCCGGCGAACTGCCTTCTGCTTTCGTTGTCA   1450
AGCAGCCTGGTACAGAAATTACCGCCAAAGAAGTGTATGATTACCTGGCT   1500
GAACGTGTGAGCCATACTAAGTACTTGCGTGGCGGCGTGCGTTTTGTTGA   1550
CTCCATCCCTCGTAACGTAACAGGCAAAATTACCCGCAAGGAGCTGTTGA   1600
AACAATTGTTGGTGAAGGCCGGCGGT                           1626
```

SEQ ID NO: 301

GRver5.1 protein sequence of pGL3 vectors

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MVKREKNVIYGPEPLHPLEDLTAGEMLFRALRKHSHLPQALVDVVGDESL    50
SYKEFFEATVLLAQSLHNCGYKMNDVVSICAENNTRFFIPVIAAWYIGMI   100
VAPVNESYIPDELCKVMGISKPQIVFTTKNILNKVLEVQSRTNFIKRIII   150
LDTVENIHGCESLPNFISRYSDGNIANFKPLHFDPVEQVAAILCSSGTTG   200
LPKGVMQTHQNICVRLIHALDPRVGTQLIPGVTVLVYLPFFHAFGFSITL   250
GYFMVGLRVIMFRRFDQEAFLKAIQDYEVRSVINVPSVILFLSKSPLVDK   300
YDLSSLRELCCGAAPLAKEVAEVAAKRLNLPGIRCGFGLTESTSANIHSL   350
RDEFKSGSLGRVTPLMAAKIADRETGKALGPNQVGELCIKGPMVSKGYVN   400
NVEATKEAIDDDGWLHSGDFGYYDEDEHFYVVDRYKELIKYKGSQVAPAE   450
LEEILLKNPCIRDVAVVGIPDLEAGELPSAFVVKQPGKEITAKEVYDYLA   500
ERVSHTKYLRGGVRFVDSIPRNVTGKITRKELLKQLLEKAGG          542
```

SEQ ID NO: 298

RDver5.1 protein sequence of pGL3 vectors

```
MVKREKNVIYGPEPLHPLEDLTAGEMLFRALRKHSHLPQALVDVVGDESL    50
SYKEFFEATVLLAQSLHNCGYKMNDVVSICAENNTRFFIPVIAAWYIGMI   100
VAPVNESYIPDELCKVMGISKPQIVFTTKNILNKVLEVQSRTNFIKRIII   150
LDTVENIHGCESLPNFISRYSDGNIANFKPLHFDPVEQVAAILCSSGTTG   200
LPKGVMQTHQNICVRLIHALDPRYGTQLIPGVTVLVYLPFFHAFGFHITL   250
GYFMVGLRVIMFRRFDQEAFLKAIQDYEVRSVINVPSVILFLSKSPLVDK   300
YDLSSLRELCCGAAPLAKEVAEVAAKRLNLPGIRCGFGLTESTSAIIQSL   350
RDEFKSGSLGRVTPLMAAKIADRETGKALGPNQVGELCIKGPMVSKGYVN   400
NVEATKEAIDDDGWLHSGDFGYYDEDEHFYVVDRYKELIKYKGSQVAPAE   450
LEEILLKNPCIRDVAVVGIPDLEAGELPSAFVVKQPGKEITAKEVYDYLA   500
ERVSHTKYLRGGVRFVDSIPRNVTGKITRKELLKQLLEKAGG          542
```

SEQ ID NO: 300

RD1561H9 protein sequence of pGL3 vectors

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MVKREKNVIYGPEPLHPLEDLTAGEMLFRALRKHSHLPQALVDVVGDESL    50
SYKEFFEATVLLAQSLHNCGYKMNDVVSICAENNTRFFIPVIAAWYIGMI   100
VAPVNESYIPDELCKVMGISKPQIVFTTKNILNKVLEVQSRTNFIKRIII   150
LDTVENIHGCESLPNFISRYSDGNIANFKPLHFDPVEQVAAILCSSGTTG   200
LPKGVMQTHQNICVRLIHALDPRYGTQLIPGVTVLVYLPFFHAFGFHITL   250
GYFMVGLRVIMFRRFDQEAFLKAIQDYEVRSVINVPSVILFLSKSPLVDK   300
YDLSSLRELCCGAAPLAKEVAEVAAKRLNLPGIRCGFGLTESTSAIIQTL   350
GDEFKSGSLGRVTPLMAAKIADRETGKALGPNQVGELCIKGPMVSKGYVN   400
NVEATKEAIDDDGWLHSGDFGYYDEDEHFYVVDRYKELIKYKGSQVAPAE   450
LEEILLKNPCIRDVAVVGIPDLEAGELPSAFVVKQPGTEITAKEVYDYLA   500
ERVSHTKYLRGGVRFVDSIPRNVTGKITRKELLKQLLVKAGG          542
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SEQ ID NO: 302